

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 04:31:04 ; Search time 11423 Seconds

(without alignments)
11553.842 Million cell updates/sec

Title: US-09-430-412A-1

Perfect score: 3045
Sequence: 1 atccatcaataatccgtta.....gtggagatggggtcttcg 3045

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_ov.*
5: gb_ov.*
6: gb_ov.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sfs.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_hum.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_mu.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sfs.*
28: em_un.*
29: em_vl.*
30: em_hcg_hum.*
31: em_hcg_inv.*
32: em_hcg_other.*
33: em_hcg_mus.*
34: em_hcg_pln.*
35: em_hcg_rod.*
36: em_hcg_mam.*
37: em_hcg_vrt.*
38: em_sy.*
39: em_hlgo_hum.*
40: em_hlgo_mus.*
41: em_hlgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2731	89.7	139929	9	AC008965	AC008965 Homo sapi
2	2731	89.7	180483	9	AC122707	AC122707 Homo sapi
3	1959.2	64.3	3000	6	AX194837	AX194837 Sequence
4	979.4	32.2	3001	6	AX194838	AX194838 Sequence
5	747.8	24.6	1204	6	HS5HT1A	21168 H.sapiens 5
6	522.4	17.2	2512	6	AX194847	AX194847 Sequence
7	438	14.4	468	9	HS5HT1A5	X53826 H.sapiens D
8	163.6	5.4	3635	10	AF087675	AF087675 Rattus no
9	162.6	5.3	203941	2	AC114573	AC114573 Mus muscu
10	159.6	5.2	259367	2	AC130951	AC130951 Rattus no
11	159.6	5.2	260103	2	AC094978	AC094978 Rattus no
12	144	4.7	5570	10	AY029704	AY029704 Mus muscu
13	139.6	4.6	2725	10	AF217200	AF217200 Rattus no
14	134.2	4.4	1256	10	MM032820	U33820 Mus musculu
15	125.6	4.1	7218	6	166494	166494 Sequence 14
16	100	3.3	158659	9	AP006183	AP006183 Homo sapi
17	95	3.1	133877	2	AC120883	AC120883 Homo sapi
18	94	3.1	129240	9	AC084128	AC084128 Homo sapi
19	94	3.1	170928	9	AC034148	AC034148 Homo sapi
20	92	3.0	160732	9	AC018647	AC018647 Homo sapi
21	91.8	3.0	169122	9	AC106803	AC106803 Homo sapi
22	91.6	3.0	67970	3	PFMAL1P3	AL031746 Plasmodiu
23	91.2	3.0	148075	3	AC110014	AL031746 Plasmodiu
24	91.2	3.0	250029	3	AE014816	AC110014 Homo sapi
25	90.2	3.0	76568	3	MBREV	AE014816 Plasmodiu
26	90	3.0	139409	9	AC069181	AF538053 Monosiga
27	89.2	2.9	8056	6	AX599046	AC069181 Homo sapi
28	89	2.9	178207	9	AC140172	AX599046 Sequence
29	89	2.9	258658	3	AE014832	AC140172 Homo sapi
30	88.8	2.9	133877	2	AC120883	AE014832 Plasmodiu
31	88.6	2.9	108902	2	AC011430	AC120883 Homo sapi
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36	87.8	2.9	169546	2	AC004157	AC005504 Plasmodiu
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38	87.8	2.9	250421	3	AE014849	AL162191 Human chr
39	87.6	2.9	2687	3	PFAPKA	AE014849 Plasmodiu
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41	87.2	2.9	143331	9	AC091214	AC096750 Homo sapi
42	87.2	2.9	271546	3	AE014843	AC091214 Homo sapi
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTD-2364L17, complete sequence.
AC008965
VERSION AC008965.6 GI:15042790
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 139939)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
Unpublished

Pred. No. is the number of results predicted by chance to have a

REFERENCE 2 (bases 1 to 139939)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 139939)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 On Jul 31, 2001 this sequence version replaced gi:9256099.
 COMMENT Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.hgsc.stanford.edu
 Quality: Phrap Quality >=40 99.5% of Sequence;
 Estimated Total Number of Errors is 0.5.
 STS Content:
 SHGC-105347 G58762
 SHGC-105921 G58845

FEATURES
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 /db_xref="taxon:9606"
 /chromosome="15"
 /clone="CTD-2364117"

ORIGIN

Query Match 89.7%; Score 2731; DB 9; Length 139939;
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 Matches 2984; Conservative 5; Mismatches 45; Indels 29; Gaps 20;

QY 1 ATGATCAATATATCCGTTATTAAGCTGTTTCTTACGTTAACTTTAGAGCCTTGA 60
 Db 95355 ATGATCAATATATCCGTTATTAAGCTGTTTCTTACGTTAACTTTAGAGCCTTGA 95296
 QY 61 AGAATAAGAGCTCATCTCTTAA--CAGAGCTTTGGTTGCAGACCTTACTTAAGAATA 118
 Db 95295 AGAATAAGAGCTCATCTCTTAA--CAGAGCTTTGGTTGCAGACCTTACTTAAGAATA 95236
 QY 119 TTGGTATTTCTGATCTTTAAGGTTAAACATGAAAGAAATGGCTTAAGGAAATGAATG 178
 Db 95235 TTGGTATTTCTGATCTTTAAGGTTAAACATGAAAGAAATGGCTTAAGGAAATGAATG 95177
 QY 179 AAAGCATATCATCTGAT 237
 Db 95176 AAAGCATATCATCTGAT 95117
 QY 238 AAGTTAAACATTAATATCTAT 297
 Db 95116 AAGTTAAACATTAATATCTAT 95058
 QY 298 GAATTAATCTGATATCTGTTTCCCTCCAGATATCAATAGTGGCCTTGAAGAACTT 357
 Db 95057 ATA--CTTCAATCTGTTTCCCTCCAGATATCAATAGTGGCCTTGAAGAACTT 95002
 QY 358 TTAATTTGTAAGAAATTAATGTTTGAATATATATATATATATATATATATATATATATAT 417
 Db 95001 TTAATTTGTAAGAAATTAATGTTTGAATATATATATATATATATATATATATATATATAT 94942
 QY 418 GAATTAATCTGATATCTGTTTCCCTCCAGATATCAATAGTGGCCTTGAAGAACTT 477
 Db 94941 GAATTAATCTGATATCTGTTTCCCTCCAGATATCAATAGTGGCCTTGAAGAACTT 94883
 QY 478 AATAACAAATGCTATACCTCAGAAATATTAATCCAGATTTTACAGATTTTAACTTTCT 537
 Db 94882 AATAACAAATGCTATACCTCAGAAATATTAATCCAGATTTTACAGATTTTAACTTTCT 94823
 QY 538 TGATGAGAAATTAATTTGCTCATTTATTAACCTATTT--GATCCAAAGATGAAGAGA 596
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 QY 657 GACCAAACTTTAATTAATGATTTTACATTAATTAATGATTTTACATTAATTAATGATTT 716
 Db 94702 GACCAAACTTTAATTAATGATTTTACATTAATTAATGATTTTACATTAATTAATGATTT 94643
 QY 717 CTTTATTTTACTTTGTTTATGATGTCATTAATTAATTTCAAGATTTAATTTAGATTAATTC 776
 Db 94642 CTTTATTTTACTTTGTTTATGATGTCATTAATTAATTTCAAGATTTAATTTAGATTAATTC 94583
 QY 777 AGCCTTTAATTAATTTTCCATTAATTAATTTTGGACCTCTTAATTTTAACTTTAATTTA 836
 Db 94582 AGCCTTTAATTAATTTTCCATTAATTAATTTTGGACCTCTTAATTTTAACTTTAATTTA 94525
 QY 837 ATATAGTCTGATATTTGGAAGAGACTTTAGAGTGAATGAATAGATTAATTTCAAACTTT 896
 Db 94524 ATATAGTCTGATATTTGGAAGAGACTTTAGAGTGAATGAATAGATTAATTTCAAACTTT 94465
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 Db 94464 -AAAGACTTCTTCAAGCTCTGTAACAGCATTAACATTAATTTACTTATCTTTCTTTTC 94405
 QY 956 ATGCC---ATGATCATCAGATGATGCTCATGTTGGTGCATGCTG--AATGATTAAGT 1010
 Db 94404 ATGCCATCATCAGATGATGCTCATGTTGGTGCATGCTG--AATGATTAAGT 94345
 QY 1011 GGGACTGTGCC---AGCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1066
 Db 94344 GGGAACTGTGCCAGCTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 94285
 QY 1067 CACGTGCTGATATGTAATGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 1126
 Db 94284 CACGTGCTGATATGTAATGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 94225
 QY 1127 CTCTTTTGTGTTGGGCTTGAAGATTAAGAGCTATGAATTAATTAATTAATTAATTAATTA 1186
 Db 94224 CTCTTTTGTGTTGGGCTTGAAGATTAAGAGCTATGAATTAATTAATTAATTAATTAATTA 94165
 QY 1187 AATATTAAGATTTATGCAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1246
 Db 94164 AATATTAAGATTTATGCAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 94105
 QY 1247 TTGAATTTGATTTCTTCACTCAGGATGATGATGATGATGATGATGATGATGATGATGAT 1306
 Db 94104 TTGAATTTGATTTCTTCACTCAGGATGATGATGATGATGATGATGATGATGATGATGAT 94045
 QY 1307 TGGTATGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365
 Db 94044 TGGTATGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 93985
 QY 1366 AATTTG--TTTCTGTTAAAGGAACAGCTTGAACAAACCTTTGATGATGATGATGATGAT 1423
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 QY 1424 TCAAGATTTTAACTTTCCAAATGTTAATCATTTGGAATTAATGATGATGATGATGATGAT 1483
 Db 93924 TCAAGATTTTAACTTTCCAAATGTTAATCATTTGGAATTAATGATGATGATGATGATGAT 93865
 QY 1484 CCAACAAAGGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1543
 Db 93864 CCAACAAAGGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 93805
 QY 1544 ACAGGTGAATGTTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1603
 Db 93804 ACAGGTGAATGTTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 93745
 QY 1604 GACGATTTCTTCAAGCTTTGGAAGAGCTTAATTAATTAATTAATTAATTAATTAATTA 1663
 Db 93744 GACGATTTCTTCAAGCTTTGGAAGAGCTTAATTAATTAATTAATTAATTAATTAATTA 93685
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Qy 119 TTGGATATCTGATCTTTAAGATTAAACATAGAGAAATGGCTAGTGAATAATG 178
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Qy 179 AAAGCAATATCATCTGATATATCATATTTATTAATATCATGATTTATTAAGTTT-AA 237
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Qy 238 AAGTTAAACATTAATATCATATATGATGATGATGATGATGATGATGATGATGATG 297
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Qy 298 GAATATCTTGCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 357
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Qy 358 TTTAAATGTAAGAAATTAATGTTGATATATATGATATATATATATATATATATAT 417
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Qy 418 GAATATCTTGCATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG 477
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Db 100596 AATAAATAATGATATATATATATATATATATATATATATATATATATATATATAT 100655
Qy 538 TGATGAGAAAAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 596
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Db	102572	CCATCAATTAGCAATAATTGGAGACAGACCCAGACCTGTTCACCTTCCATTCCAGGCTC	102633	
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QY	2683	TCTGTGTGTGTAAGTAGTGAATTCGATCTCTGTTCGCAAAAAGAGACTCGAATGCAAGA	2742	
Db	102812	TCTGTGTGTGTAAGTAGTGAATTCGATCTCTGTTCGCAAAAAGAGACTCGAATGCAAGA	102877	
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Db	102872	CGCTGACCTTGAGGAGAGAGAGGCGCGGACCCACAGGAAAGAGCACTTCTCGGGTTG	102933	
QY	2803	GCGAGATATTAGAGGGGAGCGGTTAAGTGGGAGGAAAGAGACCTTGCTTCAAGGACAC	2862	
Db	102932	GCGAGATATTAGAGGGGAGCGGTTAAGTGGGAGGAAAGAGACCTTGCTTCAAGGACAC	102997	
QY	2863	TCACAGAGGATTAATTAAGAGGAGGTGAGAGAGGAGAGGAGACTGAAAGGAAAGCAGG	2922	
Db	102992	TCACAGAGGATTAATTAAGAGGAGGTGAGAGAGGAGAGGAGACTGAAAGGAAAGCAGG	103051	
QY	2923	TGGGGAAGAAAGGGGAGCAAAAGAGGACGAAAGAGAGAGAGAGAGAGGAGGAGGA	2982	
Db	103052	TGGGGAAGAAAGGGGAGCAAAAGAGGACGAAAGAGAGAGAGAGAGAGGAGGAGGA	103111	
QY	2983	GAGGGAAGAAAGAAATAGGAGAGAGAGGAGTCAACAGAGTGAACCTGTGAGAGATGGGGCTTC	3042	
Db	103112	GAGGGAAGAAAGAAATAGGAGAGAGAGGAGTCAACAGAGTGAACCTGTGAGAGATGGGGCTTC	103177	
QY	3043	TCG 3045		
Db	103172	TCG 103174		
RESULT 3	AX194837/c	3000 bp	DNA	linear
LOCUS	AX194837	Sequence 307 from Patent WO0151659.		PAT 28-Aug-2001
DEFINITION	AX194837			
ACCESSION	AX194837.1	GI:15385484		
VERSION	AX194837.1			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1	Chen, T., Blumenfeld, M. and Cohen, D.		
AUTHORS	Blalistic markers derived from genomic regions carrying genes			
TITLE	Involved in central nervous system disorders			

```

JOURNAL          Patent: WO 0151659-A 307 19-JUL-2001;
GENSET          (PR)
FEATURES
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1. *Chlorophyll a* (Chl a) is the primary photosynthetic pigment in most plants and algae. It is a green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl a is essential for the light-dependent reactions of photosynthesis, where it converts light energy into chemical energy.

2. *Chlorophyll b* (Chl b) is an accessory pigment found in green plants and algae. It is a yellow-green pigment that absorbs light energy in the blue and red regions of the visible spectrum. Chl b transfers energy to Chl a, which then uses it for photosynthesis.

3. *Carotenoids* are a group of pigments that include carotenes and xanthophylls. They are responsible for the yellow, orange, and red colors seen in autumn foliage. Carotenoids absorb light energy in the blue and green regions of the visible spectrum and transfer energy to Chl a.

4. *Xanthophylls* are a type of carotenoid that are responsible for the yellow color seen in autumn foliage. They absorb light energy in the blue and green regions of the visible spectrum and transfer energy to Chl a.

5. *Anthocyanins* are water-soluble pigments that are responsible for the red, purple, and blue colors seen in autumn foliage. They are produced by the plant's own chemical processes and are not directly involved in photosynthesis.

6. *Flavonoids* are a group of pigments that include flavones and flavanols. They are responsible for the yellow and orange colors seen in autumn foliage. Flavonoids absorb light energy in the blue and green regions of the visible spectrum and transfer energy to Chl a.

7. *Anthoxanthins* are a type of flavonoid that are responsible for the yellow color seen in autumn foliage. They absorb light energy in the blue and green regions of the visible spectrum and transfer energy to Chl a.

8. *Anthocyanins* are water-soluble pigments that are responsible for the red, purple, and blue colors seen in autumn foliage. They are produced by the plant's own chemical processes and are not directly involved in photosynthesis.

9. *Anthocyanins* are water-soluble pigments that are responsible for the red, purple, and blue colors seen in autumn foliage. They are produced by the plant's own chemical processes and are not directly involved in photosynthesis.

10. *Anthocyanins* are water-soluble pigments that are responsible for the red, purple, and blue colors seen in autumn foliage. They are produced by the plant's own chemical processes and are not directly involved in photosynthesis.

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1980

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Dd	2180	TAAATPACTGTCTCTCTCTTTCTAAGAAGTGTTGAATTTCTCAATACTGTCTTCATTTCT	2121
OY	1801	GGCATTAAGGGATTTCCAGATGGCACTCTAAAACATTTGCCAGAAAGTGGCGAACATAAAC	1860
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OY	1861	CTCATTTGCTTGAACCTGTCCCAGAGTGTCAAACCAGTTTCTGAATTTAAGAGAGGCTAGC	1920
Dd	2062	CTCATTTGCTTGAACCTGTCCCAGAGTGTCAAACCAGTTTCTGAATTTAAGAGAGGCTAGC	2003
OY	1921	CGGCTAGCGAACCGGGATTTCCACCAAGTTTCCCCAGAGGTTTGACGGCTCTGGTAAGAA	1980
Dd	2002	CGGCTAGCGAACCGGGATTTCCACCAAGTTTCCCCAGAGGTTTGACGGCTCTGGTAAGAA	1943
OY	1981	GTGCAAAAGCCCATGTGAATATCCAGSGCTTCACTTAGAACACATATGCAAAATATTTCCA	2040
Dd	1942	GTGCAAAAGCCCATGTGAATATCCAGSGCTTCACTTAGAACACATATGCAAAATATTTCCA	1883
OY	2041	TCCCGAATTTTACTAGCCACAAGGTATAGGGAAGGAGAGAGTCACTGAATTTCAAGTG	2100
Dd	1882	TCCCGAATTTTACTAGCCACAAGGTATAGGGAAGGAGAGTCACTGAATTTCAAGTG	1823
OY	2101	TAGTAGTATGGMAAGTGTGTGTGTATTAGAAATATATCACACTGAGTTTTGTTCTT	2160
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OY	2161	CATTTCGAGATGCAATTTGTTTAACTCTCTCTGTCTTTGACAGTCCCTTAATTTTCGT	2220
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OY	2281	AAAGCTGGACTGTATGATGATTAACGGAAGTACCGTTTGTGTGTGTGTGTCTGTCTTCTC	2340
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OY	2700	AGTTCTGACTCTCTGTTGCAAAAAGAGCTCGAATGCCAAGACGCTGAGCTAAGGGAG	2759
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Dd		1102	GAGGGTTAAGATGGGAGAGGAAGACCTGGCTTTTCCAAAGGACTGCACAGAGCGATTAAATA	1043
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Dd		1042	AAGGGAAGTGTGGGAGGAAGAGCGGACACTGTAAGGAAGGAAGCAGAGTGGGAGAAAGGGGAC	983
Oy		2940	AAAAGAGCAGAGAAGAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAAT	2999
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DEFINITION	Sequence 308 from Patent WO0151659.			
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VERSION	AX194838.1		GI:15385465	
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ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1			
AUTHORS	Chu, T., Blumenfeld, M. and Cohen, D.			
TITLE	Biallelic markers derived from genomic regions carrying genes involved in central nervous system disorders			
JOURNAL	Patent: WO 0151659-A 308 19-JUL-2001;			
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Oy		2149	AGTTTTGTTCTTCATTTGAGATGAGTGTTCCTCTGTCCTTTGACAGCTCT	2208
Dd		129	AGTTTGTCTTCATTTGAGATGAGTGTTCCTCTGTCCTTTGACAGCTCT	188
Oy		2209	TTATATTTTCGTTCTCTCCCGTTCCCCAACGTTAAAAAAAAGTCACAGGCAATATTTCT	2266
Dd		169	TTATATTTTCGTTCTCTCCCGTTCCCCAACGTTAAAAAAAAGTCACAGGCAATATTTCT	248
Oy		2269	CCCTGAGGAGATTAAGCTGACGTGTAGATATATAACGAGGTACCGTTTGTGTGTGTG	2322

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Query Match	24.6%	Score 747.8; DB 9; Length 1204;
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Matches 774;	Conservative 0;	Mismatches 7; Indels 2; Gaps 2;
Db	1	ATTCTCCCTGAGGAGTAAAGGCTGAGCTGATATATAGCGAGGTACCGTTTGTGT 2323
2264	ATTCTCCCTGAGGAGTAAAGGCTGAGCTGATATATAGCGAGGTACCGTTTGTGT 2323	
2324	TGTTGCGCGTGTGCTGTTTGTGTTTGGAGAGGAGTCTGCTGTGCGCCAGAGCTG 2383	
Db	61	TGTTGCGCGTGTGCTGTTTGTGTTTGGAGAGGAGTCTGCTGTGCGCCAGAGCTG 120
2384	AGTGCATATGCGCGAGAAACGAGGATGCTTTTAAATTAAGACACACTCGGCTCTT 2443	
Db	121	AGTGCATATGCGCGAGAAACGAGGATGCTTTTAAATTAAGACACACTCGGCTCTT 180
2444	CCATCAATTAGCAATATTGGAGACATGACCCAGAGCTGTACCTGCCATTCCAGGCT 2503	
Db	181	CCATCAATTAGCAATATTGGAGACATGACCCAGAGCTGTACCTGCCATTCCAGGCT 240
2504	CCATGCTCTCTTCTCATCTCTATATGGCACTCGGATGCTGACAGATTAAAGAT 2563	
Db	241	CCATGCTCTCTTCTCATCTCTATATGGCACTCGGATGCTGACAGATTAAAGAT 300
2564	TGAGGAGATTAATTAAGAGCAAGAGTGTGGAATTCCTCCGCCAAGTTTCCAAACC 2623	
Db	301	TGAGGAGATTAATTAAGAGCAAGAGTGTGGAATTCCTCCGCCAAGTTTCCAAACC 360
2624	CAGTTTGTGCTGAGTGGAGGCGAGATTATTTGTACAACCTTGGTCTGACCGGCA -GGA 2682	
Db	361	CAGTTTGTGCTGAGTGGAGGCGAGATTATTTGTACAACCTTGGTCTGACCGGCAAGGA 420
2683	TCTGGTGTGTAAGAGTGTGAGCTCTGTGCAAAAAGAGTCTGAAATGCAAGA 2744	
Db	421	CCTGCTGTGTGAATGATGTTCTGAGCTCTGTGCAAAAAGAGTCTGAAATGCAAGA 480
2743	CGCTGAGCTAAGAGAGAGGCGGAGACCCAGAGAAAGAGCACTCTCGCGAGTTG 2802	

Db		481	CGCTGAGCTTGAAGAGAGAGAGAGGGCCGGGACCCAGAGAAAGAGCACTTCCTCGGGTTTG	540
OY		2803	GGGAAATATTATGAGAGGGGAGGGTTTGAAGTGGAGGGAAGAGCCTTGCTTTTGGAAAGCCAG	2862
Db		541	GGGAAGATATTAGAGAGGGAGGGTTTGAAGTGGAGAGGAAAGAG-CTGCTTTGGAAAGCAG	599
OY		2863	TCACAGAGGGATTAATAAAGAGGAACTGAGAGGAAGAAGGAGCATGAAAAGGAGAGGCAGG	2922
Db		600	TCAcAGAGGGATTAATAAAGAGGAAGTAGAGAGGAAGAAGGGAGACTTTAAAGGAGAGGCAGG	659
OY		2223	TGGGGAGAAAGGGGGAGCGAAAGAGGAGCAAGAAAGAGAAAGAGAGAGAGAGAGAGGGGGAGAG	2982
Db		660	TGGGAGAAAGGGGGAGCGAAAGAGGAGCAAGAAAGAGAAAGAGAGAGAGAGAGGGGGAGAG	719
OY		2983	GAGGAGAGAGGAAGGAATAATGAGAGAGAGAGGTCAcAGAGTAGCCGTGAGAGATGAGGCTTC	3042
Db		720	GAGGAGAGGAAGGAATAATGAGAGAGAGAGGTCAcAGAGTAGCCGTGAGAGATGAGGCTTC	779
OY		3043	TCG 3045	
Db		780	TCG 782	
RESULT 6				
AX194847 LOCUS 2512 bp DNA linear PAT 28-AUG-2001				
DEFINITION Sequence 317 from Patent WO0151659.				
VERSION AX194847 GI:15385494				
KEYWORDS				
SOURCE				
ORGANISM Homo sapiens (human)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1	Chu,T., Blumenfeld,M. and Cohen,D.		
AUTHORS		Biallelic markers derived from genomic regions carrying genes		
TITLE		Involved in central nervous system disorders		
JOURNAL		Patent: WO 0151659-A 317 19-JUL-2001;		
FEATURES		Location/Qualifiers		
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	misc_feature	1482..1500		
		/note="99-5069-331.mis1"		
	misc_feature	1489..1513		
		/note="99-5069-331 potential probe"		
	variation	1501		
		/note="99-5069-331 : polymorphic base C or T"		
	misc_feature	1502..1521		
		/note="99-5069-331.mis2, potential complement"		
	primer_bind	1702..1719		
		/note="downstream amplification primer, complement"		
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Query Match		17.2% Score 522.4 DB 6 Length 2512:		
Best Local Similarity		98.6%; Pred No.1,9e-81;		
Matches 548:		Mismatches 6; Indels 2; Gaps 2;		
OY	2491	CCCATTCAGGCTCCCTATGCTCTCTTTCTCATCTCCTATTCGACTCTGGATGCTGAC	2556	
Db	1	CCCATTCAGGCTCCCTATGCTCTCTTTCTCATCTCCTATTCGACTCTGGATGCTGAC	60	
OY	2551	ACGATTAAAGAAATTTGGCAGATATATATAGGACAAGAGTAGTTGSAATCCCTCCGCCAA	2610	
Db	61	ACGATTAAAGAAATTTGGCAGATATATATACCACCAAGAGTAGTTGGAATTCCTCCCCCAA	120	
OY	2611	GTTTTTCACACCCCAAGTTTGTCTGAGTTGAGAGCGAGATTATTTGTATCACCTTGTGTC	2670	

Db	121	GTTTTCCACCCAGTTTGTCTGGTTGAGGCGAGTTTATTGTTACAACTTGGTC	180
QY	2671	TGACCGGCA - GGATCTGGTGTGTGAAGTAGATTCTAGTCTCTGTTGACAAAAGAGAC	2729
Db	181	TGACCGGCGAGGAGCTGGTGTGTGTAGTAGTAGTTCTGAGCTCTGTTGACAAAAGAGAC	240
QY	2730	TGGATGCAAAAGCGCTGAGCTAAGGAGAAAGAGGGCGGGAGCCCAAGAGAAAGAGCA	2789
Db	241	TGAAATGCAAAAGCGCTGAGCTAAGGAGAAAGAGGGCGGGAGCCCAAGAGAAAGAGCA	300
QY	2790	CTCCTCGGGGCTTGGGGAAGTATTAGAGGGAGGGTTAGATGAGGAGGAAGAGCTGG	2849
Db	301	CTCCTCGGGGCTTGGGGAAGTATTAGAGGGAGGGTTAGATGAGGAGGAAGAGCTGG	359
QY	2850	CTTTCGAAAGCGACTCAGAGGAGTAATAATAAGGAAGTGAAGAGGAAGAGGAGACTGA	2909
Db	360	CTTTCGAAAGCGACTCAGAGGAGTAATAATAAGGAAGTGAAGAGGAAGAGGAGACTTA	419
QY	2910	AAGGGAGGCGAGTGGGGAAGAAAGGGGGACGAAAGAGCGAAGAGAGAAAGAGAGAG	2968
Db	420	AAGGGAGGCGAGTGGGGAAGAAAGGGGGACGAAAGAGCGAGAGAGAGAAAGAGAGAG	479
QY	2970	AAGAGAGGGGAGAGAGGGAAGGAAGGAATAATGAGAGAGAGAGGCTCAGAGTGAACGGAG	3029
Db	480	AGAAGAGGGGAGAGAGGGAAGGAATAATGAGAGAGAGAGGCTCAGAGTGAACGGAG	539
QY	3030	AGGATGGGCTTCTCG 3045	
Db	540	AGGATGGGCTTCTCG 555	

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RESULT 7
LOCUS      HS5HT1A.RS               699 bp    DNA             linear      PRI 12-JUL-1994
DEFINITION H.sapiens DNA 5' to 5HT1A receptor gene.
ACCESSION  X53826
VERSION     X53826.1
KEYWORDS    GI:510982
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS     1 (bases 1 to 699)
            Potts,W.J., Morten,J., Elvin,P., Deakin,W., Braude,W.M.,
            Waring,H.J. and Jenner,D.E.
TITLE       Sequence 5' to the gene for human 5HT1A receptor obtained by
            "vectorette" walking
JOURNAL     2 (bases 1 to 699)
REFERENCE   2 (bases 1 to 699)
AUTHORS     Jenner,D.E.
TITLE       Direct Submisson
JOURNAL     Submitted (30-JUN-1990) D.E. Jenner, ICI PHARMACEUTICALS, ALDERLEY
            PARK, MACCLESFIELD, CHESHIRE, SK10 4TG, UK
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                    /db_xref="taxon:9606"
                    /chromosome="5"
                    /map="Sg11-5q13"
                    506..621
                    /note="palindrome"
                    /rpt_type=INVERTED
                    681..696
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                    /rpt_type=INVERTED
ORIGIN
Query Match      14.4%; Score 438; DB 9; Length 699;
Best Local Similarity 99.8%; Pred. No. 1,3e-66;
Matches 449; Conservative 0; Mismatches 0; Indels 1; Gaps 1.

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QY 2596 AATTCCTCCGCCAAGTTTTCACACCCAGTTTGTGGTTGAGGCGGAGTTATT 2655
 DB 23 AATTCCTCCGCCAAGTTTTCACACCCAGTTTGTGGTTGAGGCGGAGTTATT 82
 QY 2656 GTTACAACTTGTGCTGACCCGAGGATCTGTGTGTGTAAAGTATTTCTGT 2715
 DB 83 GTTACAACTTGTGCTGACCCGAGGATCTGTGTGTGTAAAGTATTTCTGT 142
 QY 2716 TGACAAAAAGACTTCGAAATCGAAGCGCTGAGCTGAGGAGAGAGGCGGAGACC 2775
 DB 143 TGACAAAAAGACTTCGAAATCGAAGCGCTGAGCTGAGGAGAGAGGCGGAGACC 202
 QY 2776 AGAGAAAAGAGCACTCTCCGAGTGTGGGAAATTAAGAGGAGGCTTGAAGTGG 2835
 DB 203 AGAGAAAAGAGCACTCTCCGAGTGTGGGAAATTAAGAGGAGGCTTGAAGTGG 262
 QY 2836 GGGAAAGAGCTGTGCTTTCGAAAGCACTCAGAGAGGATTAATTAAGGAAATGAGAGG 2895
 DB 263 GGGAAAGAGCTGTGCTTTCGAAAGCACTCAGAGAGGATTAATTAAGGAAATGAGAGG 322
 QY 2896 AAGAGGAGAGCTGAAAGGAAAGGAGTGGGAGAGAGGAGGAGGAGGAGAGG 2955
 DB 323 AAGAGGAGAGCTGAAAGGAAAGGAGTGGGAGAGAGGAGGAGGAGGAGGAGG 382
 QY 2956 GAGAAAGAGAGAGAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3015
 DB 383 GAGAAAGAGAGAGAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 441
 QY 3016 CAGAGTGAACCTGGAGAGATGGGGCTTCTCG 3045
 DB 442 CAGAGTGAACCTGGAGAGATGGGGCTTCTCG 471

RESULT 9
 AF087675 3635 bp DNA linear ROD 14-FEB-2002
 LOCUS AF087675
 DEFINITION Rattus norvegicus serotonin 1A receptor gene, partial cds.
 ACCESSION AF087675
 VERSION AF087675.1 GI:3603449
 KEYWORDS
 SOURCE
 ORGANISM

Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 3635)
 Meijer, O.C., Williamson, A., Dallman, M.F. and Pearce, D.
 Transcriptional repression of the 5-HT1A receptor promoter by
 corticosterone via mineralocorticoid receptors depends on the
 cellular context
 J. Neuroendocrinol. 12 (3), 245-254 (2000)
 JOURNAL
 MEDLINE
 20189470
 PUBMED
 10718920
 REFERENCE
 2 (bases 1 to 3635)
 Meijer, O.C., Dallman, M.F. and Pearce, D.
 The rat 5-HT1A receptor promoter: activation by NGF-C, spl and
 NF-kB, and context dependent repression by corticosteroids
 unpublished
 3 (bases 1 to 3635)
 Meijer, O.C. and Pearce, D.
 Direct Submision
 Submitted (27-AUG-1998) Medicine, UCSF, 1001 Portero Avenue, San
 Francisco, CA 94110, USA
 JOURNAL
 TITLE
 location/Qualifiers
 1. 3635
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
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 /db_xref="taxon:10116"
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Query Match 5.4%; Score 163.6; DB 10; Length 3635;
 Best Local Similarity 53.9%; Pred. No. 7.4e-19;
 Matches 893; Conservative 2; Mismatches 626; Indels 135; Gaps 22;

ORIGIN
 136 TTAAGAGTTAAACATAGAAAGAAATGGCTAAG-TGAAAATGAATGAAGCAATATCATTC 194
 DB 196 TTAAGAGTTAAACATAGAAAGAAATGGCTAAGCAATGAGATGAGAGAAATGCAATACATG 255
 QY 195 TGCATATATCATTTATTTATTTATTCACAGATTTATTTAGTTTAAAGTTTAAATATAT 254
 DB 256 TGAATTTATTAATA-----ATCACAGATTTATTAAGTTTAAATACAAATAAATCATTA 309
 QY 255 CTATATGTCATTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 313
 DB 310 AATTTATTTAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 369
 QY 314 TCTGTTCCCTCCTAGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 367
 DB 370 CCAGAAATACAGAAAGCTGCTACATTTTAAAGAGAGCAAAATTTTAA 429
 QY 368 AGAAATTAATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 427
 DB 430 AGAAATTAATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 489
 QY 428 GGAATTTGAAA-----ACTTGATTAATTTTACATCATAGATAT 468
 DB 490 GAATTTCTTAACATGATTTAAACAGCTACACTGCTATTTCAAAATGATACCTCT 549
 QY 469 TGAAGCAAGATTAACAAATGCTATACCTCAGAAATATTTATTTATTTATTTATTTATTT 520
 DB 550 ATCAATTTAAATTAATTAACAAATGCTATTTATTTATTTATTTATTTATTTATTTATTT 609
 QY 521 CAGCATTTTAACTTTCTTTGAG 580
 DB 610 AAGCTTTCTAATTTTATTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 669
 QY 581 CCAACAGATTAACAGAGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 640
 DB 670 TCCAGTATTAACAGAGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 726
 QY 641 TTTACATGCTGTTTGAACCAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 695
 DB 727 TTTACATGCTGTTTGAACCAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 786
 QY 696 GCTTTCTTAAATTTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 755
 DB 787 GCTTTCTTAAATTTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 843
 QY 756 AAGTTTAAATTTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 815
 DB 844 AAGTTTCTCTTGAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 898
 QY 816 CTAACTATTTTAACTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 875
 DB 899 GGAATTAATTTTAACTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 955
 QY 876 ATAGATCTTCAAGATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 935
 DB 956 CTACATGCTCAAGATTTTAAAG 1008
 QY 936 ATACTTATCTTTCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 995
 DB 1009 AAGATGCTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1068
 QY 996 GCTGATATTTGATGAG 1055
 DB 1069 ATTCATTAATGATGAG 1109

Best Local Similarity 54.9%; Pred. No. 1.7e-18; Matches 704; Conservative 0; Mismatches 484; Indels 94; Gaps 16;

Qy	475	AAAGATACAAAGCTTACCTGAGAAATTAATTCAGATTTTACGATTTTACTT	534
Db	112977	AAAGCAATCCAGATTAATAGATATTAACATAAATCTGACATCAAGCTCTTAATTT	113036
Qy	535	TCTTATGAGAAAAAATAATTTGTCAGTTATTAATTAATTTGGATTCACAGATGAAG	594
Db	113037	TATGAAAAAGAAAGATAGCTTTGTAGCTATTAACATAGAGATCCGATACAGAAAG	113096
Qy	595	CAGAAATCTTACATACATTTATTTATTTATTTGATTTTACATATTTACATGTGTG	654
Db	113097	GACAAATTTTACTGACAGACCTTCTGATTTGTACTAGCTATTTTACATATGCTAA	113153
Qy	655	TTGACACAAATTTTCTTATTTATTTGATTTATGATATTTGCTTCTTAATTTT	709
Db	113154	GTCGACATTTACATTTACATTTGCTTTGAGAAATACATATTTGCTTTTGAATGTA	113213
Qy	710	AAGTTTCTTATTTTACTTTGTTATTTAGTCTCAATTAATTTCAAGTTTATTTAG	769
Db	113214	CA---TGTTCTTCTTCTTCTTCTGATGCTTGCCACATTTTAAAGTTTCTCTTG	113270
Qy	770	ATAATGACCTTTTAAATATTTTCCATTAATTTTGGACCTTACCTATTTTA	829
Db	113271	GAAATTTTATGATTTAGCAT---CCATTAATTTCTCTG-CAGTTGGAATCTATTTTA	113325
Qy	830	ACTGTAATATATGATTTCTGATTTTGTGAAGACTTTGAAGTGAATATGATACCTT	889
Db	113326	A---TAAACATTTTAACTGTTGTGTGATGATTTTCTGAAACATTTACATGCTTCA	113382
Qy	890	AAATCTTAAAGACTTCTTCTGAGCTCTGTAACAGCATTTACATTTTCTTCTTT	949
Db	113383	TGTTTAAAGGCGTCTCTGAGCTCTGCTGCTGTCAGATTTGCTGCTTTGTTGGT	113442
Qy	950	CTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1009
Db	113443	GTTATGATATCCGACACATGACATGACATGACATGACATGACATGACATGACATG	113500
Qy	1010	TGGAGCTGTGCGACCTGAATTAATAAAAAAACAACAAACCTTATTCACACACAC	1069
Db	113501	-GGGACGTGTGCC-----CAAGTCAGTCATCTCTGATGATGATGATGATGATGAT	113536
Qy	1070	TGTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1129
Db	113537	AGCCCTGGGTAT-ATATTTCTGCCCACTGATCTTTTGGCTTTGATGATGATGATG	113595
Qy	1130	TTTTGTTGGCTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATG	1189
Db	113596	TTTTCTTT-GGTTTAAAGTTTCAAACTATGATGATGATGATGATGATGATGATGAT	113654
Qy	1190	ATTATGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1249
Db	113655	AGTAAAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	113714
Qy	1250	AGATGATGATTTTCCCTTACCTCAGGATGATGATGATGATGATGATGATGATGAT	1304
Db	113715	GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	113774
Qy	1305	TGTG---GTATGTTTACTGATGATGATGATGATGATGATGATGATGATGATGATG	1360
Db	113775	TGTGCTGTTTCTTTTATCTGATTAATTAAGATGATGATGATGATGATGATGATG	113831
Qy	1361	GATTAATTTGTTTCTTTGTTAAAGAAAGAGTGAACAAACCTTGTATGATGATG	1420
Db	113832	GATGCTTTTCTTTTCCAAAAATACATGATGATGATGATGATGATGATGATGATG	113891
Qy	1421	ATTATGATGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG	1480
Db	113892	TTTTCAGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	113939
Qy	1481	TCTCCAAACAAAGGTAATTTATGATGATGATGATGATGATGATGATGATGATG	1540

Db	113940	TCGCCCAATTA-----ACATGTGACTTCTATAGACAAACTGTGACACACACCA	113992
Qy	1541	AACACAGGTAAGGTGATGCTAGCTTATTTAAATGATCCAGTTGAACTTTGTG	1600
Db	113993	ATATGCCAAAATGTGTTTGTGATGATGTTCTTA-----TGAGGTGTG	114036
Qy	1601	AATGACATGATCTTACGCTTTGAGAGAGCTTAAACATATATATGCTGATTTATA	1660
Db	114037	AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	114096
Qy	1661	GGTTCAGACAAAGAGGACCTAAATTAATTTTAAAGAAATATAGAGAGACAAAA	1720
Db	114097	ACCCAGAAAAGAAAAGAAAAGAAAAGAAATGATTTGAAGAAAAAATTTAAGTGA	114156
Qy	1721	CTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1742
Db	114157	TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	114178

RESULT 12
AY029704 5570 bp .DNA linear ROD 01-SEP-2001
LOCUS
DEFINITION
Mus musculus serotonin 1A receptor gene, promoter region and partial cds.
ACCESSION
AY029704.1 GI:15418779
VERSION
AY029704
KEYWORDS
MUS MUSCULUS (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 5273 to 5560)
Parks, C.L. and Shenk, T.
The serotonin 1A receptor gene contains a TATA-less promoter that responds to Maf and Sp1
J. Biol. Chem. 271 (8), 4417-4430 (1996)
JOURNAL
MEDLINE
PUBMED
96224025
AUTHORS
Ansoerg, M., Tannenberger, C., Davies, B., Theuring, F. and Kusserow, H.
REFERENCE
2 (bases 1 to 5570)
Functional analysis of the murine 5-HT1A receptor promoter in vitro and in vivo
Unpublished
JOURNAL
REFERENCE
3 (bases 1 to 5570)
Kusserow, H., Ansoerg, M.S. and Theuring, F.
Direct Submision
Submitted (10-Apr-2001) Insititute for Pharmacology and Toxicology, Charite University Hospital, Dorotheenstr. 94, Berlin 10117, Germany

FEATURES
source
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/date="19950705"
/note="G protein coupled-receptor; 5-HT 1A receptor"
CDS
promoter
MENA
CDS

ORIGIN
Query Match 4.7%; Score 144; DB 10; Length 5570;
Best Local Similarity 48.0%; Pred. No. 1.8e-15;
Matches 1326; Conservative 0; Mismatches 1286; Indels 151; Gaps 26;

OY	357	TTTAAATTGTAAGAAATPAAAATGTTGGATATATATGTATATATATATCTAAGAAGAAAACT	416
Db	2476	TCTACATTTTTAAGAACCAAAATGTTTATATATCATGTACACTTAATTT-TGAAGATGATA	2534
OY	417	TGAATTACTTTCGATTTTGGAAAAACTTTCGAT---AAATTCATCATATAGCATAATGAAAG	473
Db	2535	TGACCTACTTGAGGAGTTTCCPAACTCGAATGTGACAAGGATACCTGTGCATATTT-AAG	2593
OY	474	CAGAGATPAACAANGCTATACCTGAGGAATATTATTCAGATTTTACAGACTTTTACT	533
Db	2594	ATATPAAATCAAACCAGACTTTATPAAACAATAAGCTTCAGACACAA-AGCCTCTTAAT	2652
OY	534	TTCTTGATGAGAAAAAATTAATTTGTCAGTATTPAACTAATTTGGATCCAAAGATGAAA	593
Db	2653	TTACTGAAAAGAAAAATGAGTTTGTATAGCTATTTAACGAATTTGGATCCAGTACAGAA	2712
OY	594	GCAGAATTTCTAAGTAACTATTTATGATTTATTTTGGATTTACATAATTTACATGTGCTG	653
Db	2713	GAAACAAT---GCTGACGTACATGTTTCCGATTTAGTACCTTAATATTTTGGCATATCTCA	2769
OY	654	TTTGACAC----AATCTTAATATAGTCTTGATATGCAATATTTGCTCTTAAATTT	708
Db	2770	CGCTGACCCATATATATCTCAAGTTGGATCTGAGATPAGAACATATTTGCTTTTGAATAT	2829
OY	709	TAAGTTCCCTTAATTTACTTTTGTTTAGTCTGACCTCACTATTAATTTCAAAGTTAATTTTA	768
Db	2830	AAATGTTCTTATTTTACTCTG-----TAGCTATAGCTACATCTTAATAATGTGTCTCT	2885
OY	769	GATAATTCAGCCCTTTAAATATATTTTCCATTAATATTTTGTGACCTTCACTATATTT	828
Db	2886	GGAATTTTGAATGTATTAAGTGT---CCCTATATATTTCTG---CAGTGCACACTATATTT	2938
OY	829	AACGTAAATATAGTTCGTATTTTGTAAGAGACTTTGAAGTGAATATAGATCCCTCA	888
Db	2939	TTTAAAAATTTTAGTCTGTGTTTGTGAGAGATTTTATCGAATATCTTACATGTTTAC	2998
OY	889	CAAACTTTAAABAGCTTCTTCAGACTGTGMAACAGATTACATGTATCTTCTT	948
Db	2999	ATGCCCTTAAAGCAATTTCTCAAGTCTGTG-----TTGCTGTGCATACCTTATGTCTA	3051
OY	949	TCTTTGCATGCAATGATCATCACAAATGATGGCTATGTGGGAGATCTCAATGATGTGA	1008
Db	3052	ATTTTGTGTATTA-----ATGCAAGCTTACAGTCTTTTC	3087
OY	1009	GTGGACCTGTGCCAGCTGAATPATAAAAAAAAAAAAAACAACAAAACCTTATCCAAACCA	1066
Db	3088	CTATCCTGAATAGATGGGGCCAACTCATCTTTGGGCACATGACCCTGATTTGTAATGT	3147
OY	1069	CTGTCTGTATTTGTAATGCATTTGGCCCCAATCGATTTCTTTTGANGCCTTGGTATGCT	1128
Db	3148	ATATGTCTGTATGTATATGTGTGACCAACGTGACTTCTTTTGATCCTTTTAGTGATTAAC	3207
OY	1129	CTTTTGTGGGCTTGAGAAATTCAGACTATGAATTCAGAGCTCAGATTTGAAACAA	1188
Db	3208	TCTTTCCTTGGTTTTAAGATTTCAAAAATNAGACATTCAAAGCTAAGATTTGAAACAA	3267
OY	1189	T-----ATTAAATTTTGGCAATCTGTAGTGAATCTGTTCATGTATATCCA	1233
Db	3268	TTTCAGATTTCTGTACACAGTAAACAATGTATAATTTGTAGTGATGCTTGGCCGTATATCTA	3327
OY	1234	GTGTCAACTGTCTTGGAGATGCAAT-----TCTTTTCACTCAGGACATGCAATCAGATG	1288
Db	3328	GAAATTAGCAGCTCTGAGATTTGCATCANGACATATGCTACCTTCABAATATGTAATCGANTC	3387
OY	1289	TATAAGTGAAA--TGTTGTGTGTAATGTTTACTGTATAGTTGCTTGAAGTCCATTTCTTAC	1346
Db	3388	TCTAAGCACAACTTTTGTGTGCTGTGTTTATTCGATTAATTAAMAATGC---CATCT	3444
OY	1347	CAATGCTCAAAATGTGATTAATATTTGTTTTCTGTTPAAAGAAAAGCCTTAGAACAAACC	1406
Db	3445	TTGTGTCAATGGAGATTAATTTTTTTTCAAAAAATHAAGS---CAGCTTAAACAAATCTC	3501
OY	1407	TTGTATGATCTCTTATTTTCAAGTGAATTAACATTTCCAAATGTAAATCATTTTGAATAATG	1466

D	b	3502	TTAGATGTCCTAAATTTAGTATCCAAATATATTTCTTTATGCAAA-----GGTAAATA	3554
O	y	1467	CAATACTATTTCGTTTCCCAACAAAAGGTAAATTTATGTCAGTTCCAAAGTTCAAGTTAT	1526
D	b	3555	CTGTGCACCAATCCCATATAAACAACCTGGATGTTCTAATAACACAAGTGTGCACCAACAC	3614
O	y	1527	GACAGCACAAAACCAACACAGGTGAAGTGTAGCCCTAGCTTTATTTAAATGCAATCCG	1586
D	b	3615	ATTAAGTAGCTGAAGAAGTGTTCGGACAGTGTCCCTAATGATTTTTTGTGAATGATATG	3674
O	y	1587	AGTTGAACCTTGATATGACAGTACTTCAGGTTTCGAAGAAGTAAACATATATATA	1646
D	b	3675	CATPAAG--CTTTCAAAAGAGCTAAAAATATCTTGACTTTGTATAAAACGAGGAAAAAA	3732
O	y	1647	GGCCTGATATATAAGTTCCAGACAAAGAAGGCACTAAATATATTTTAAAGAAAAATA	1706
D	b	3733	GGAAAAAATAATATGTTGAAGAAAAATTAAGAATCATTTAAGATTTTATTTATTT	3792
O	y	1707	GGAGAAGACAAAATCTCAATACCTGTGTCTTAAATACTGTCTTCCCTCTTCTPAAA	1766
D	b	3793	TATATATTTTACCCATTCCTTAATGCTGTGATCCCTTTAGACAGATTCCTCATGTTGTG	3852
O	y	1767	GTTGTTGTTATTTCTCATAATCTTGCTTCATTTCTGGCATPAAGGTTTCAGATGGCACTG	1826
D	b	3853	AGTGCTCCCAACCATGATATATATTTTCGTTGCTACTCTCATAGTATGATTTTGCTACTA	3912
O	y	1827	TAAACATTTGCCAGAAAGTGGGAAACATAAACCTATTCCTTAGAACCTGCCCGAGTG	1886
D	b	3913	CAAAATATTTTGGAAAGTATAGGTTCCAGAGTTGGGTTTGTATATCATTTGTTGTAATAGA	3972
O	y	1887	CTGAACCCAGTTTCTGAGATTAAGAAGGCTAGCCGAGCTAGCCAGACCGGATTCACCAA	1946
D	b	3973	TATGCTAGAGTCCTTGAGTTTCCCTTAATACTTCTTAATTTTAAATGACAAATATTTCT	4032
O	y	1947	GTTTCCCCCAGAGTTTGACAGGCTCTGCTAAGAAAGTGAAAGCCATGTGAATGTCAG	2006
D	b	4033	AAATGGGCTCTGAAGCACTTGG--CGGAAGGTGGCGCATPAACAGCTCTTACTACACA	4091
O	y	2007	GCTTCACTTGAACAACATATGCAAAATATTTCCATCCCTGAATTTACTAGCCCAAAAGCT	2066
D	b	4092	GAGCTGTCCGGGAGTGAACCCAAATTTCAAGAGACTCCGACATGCTGTGAGACAGAGAT	4151
O	y	2067	ATGGGAAGTGGCACTGTCACTGAATTAACAAGTGTACTGTATGGAAGAAAGTGATGTGT	2126
D	b	4152	GCCACTAAGTTCCCTGGAGGCTGCAGACTCCAGTGAAGAGACATPAATGTCCAAAGACA	4211
O	y	2127	GTTTAGAATATATATCACTGAAGTTTGTCTTCATTTGAGATGCAATGTTTACTCTC	2186
D	b	4212	GTAGAAAAAGAAACCATGTGTAAACATATACAGGCAAAACAATTTCTTTCACATGAATTTA	4271
O	y	2187	TCTTGTTCCTTTGACAGTCCCTTATATATTTGCTCTCCCGGTTCCCAACGTTTAA	2246
D	b	4272	TTTGCTTCATATCTATGGGAATGTATATATCATATGATATAGAGAGTGAAGTGAAGAGT	4331
O	y	2247	AAAAAGTCACAGCAATATTTCTCCCTGAGGAGTGAAGCTGTGAAGTGAATGAATACG	2306
D	b	4332	GTGATTTGGAATACACACTTAAGTGAATTTTATATTTTCTTTGAGTTTGAAGCTGTTT	4391
O	y	2307	AGATACCGTTTGTGTGTGTGTGTGTCGTGTTGCTGTTTGTATTTTGAAGACGAGTCTCG	2366
D	b	4392	TCAATCTGTCTCCAACTGTCTCTTTCTTATTTTCCCTCCATACACAGATATATATG	4451
O	y	2367	TCTGTGCGCCAGGCTGAGTGCATATGCGCGAGAACGGAAGTACGTTTATTAACATPAAG	2426
D	b	4452	AAAAGTCTACAGGACACAGATGATAGGTAAATATGTAATGAAGAACCTGTTCTTAAAGAC	4511
O	y	2427	AACAGCTCGGCTCTTCCATCATATTTAGCAATATTTGGAGACATGACCCAGACTGTCTCA	2486
D	b	4512	TGAAGCCCACTTCTTACTCTGATATATGTAAGAGGTGAAGTTTGAAGAGGTGCACTCA	4571
O	y	2487	CTTTCACATTC--AGGCTCCATAGCTTCTTTTCTCATTTCTCATTTGCCACTCTGGAGTG	2545

Db 4572 GCTTCCATCCCTCAGAGTCTCTGAGGTTTCTCTGCTGATGACCACTGTGAC 4631
 QY 2546 CTGACAGATTATTAAGATTGCGAGATPATATGAGCAAGAG----- 2588
 Db 4632 CTGGCTCTATTAAAGAGCTACAGAAATTAAGGGATCTCGGGTGGAAATATATCTT 4691
 QY 2589 -----TACTGAAATTCCTCCCTCCCAAGTTTTCMAACCCCAAGTTTGTCT 2633
 Db 4692 TCTATCTCTTCTTTATTTATTTTATTTTCTTTTGTCTTTTCTCCCTCAGTTTATA 4751
 QY 2634 GGGTTGAGGGGAGCTTATTTGTTTACACTTGTCTGACCCGAGAGATCTGTGTG 2693
 Db 4752 GGTAAAGAGCGGGGTTAGTATGTTAAACATATCTAGTACAGATCAAGATAGATA 4811
 QY 2694 T---AAGTAGTTCTGAGTCTCTGTGACAAAAGAGACTGGAATGCAAGACGCTGAGC 2750
 Db 4812 TATGAGTAGATTTCTGAGTGTGTGTG-----GACTGGAATGTAAGAGCTCCGCGC 4862
 QY 2751 TAGAGGAGAGAGAGGCGCGGAGCCAGAGAAAGAGGACCTCTCGGGGTTTGGGAAAGTA 2810
 Db 4863 TACAGGGAGAGAGGCGCGGAGCCAGAAAGAGAGGACCTCGGAGTAAAGAGTGTG 4922
 QY 2811 TTAGAGAGGAGAGGAGTTAGAGTGGAGAGAGAGCTGCTTTCGAAAGCACTCAGAG 2870
 Db 4923 GATGCGGTGGGGGTTAACTGTGGAGAGAGAGACATGCTGTCTGAGCCACACAC--AG 4980
 QY 2871 GGATTAATTAAGAGAGTGAAGAGAGAGAGAGAGAGCTGAAAGAGAGAGAGTGGGAGA 2930
 Db 4981 GACTTAAGAAAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5038
 QY 2931 AGGGGAG 2982
 Db 5039 AGCCGGAG 5088
 QY 2983 GAGGAG 3042
 Db 5089 GACAG 5158
 QY 3043 TCG 3045
 Db 5159 TGG 5161

RESULT 13
 AF217200 2725 bp DNA linear ROD 13-MAR-2000
 LOCUS AF217200 Ratrus norvegicus serotonin 5-HT1A receptor gene, partial cds.
 DEFINITION AF217200
 ACCESSION AF217200.1 GI:6969399
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Ratrus norvegicus (Norway rat)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 2725)
 Storring, J.M., Charest, A., Cheng, P. and Albert, P.R.
 TARD-diven transcriptional initiation and regulation of the rat
 serotonin 5-HT1A receptor gene
 J. Neurochem. 72 (6), 2238-2247 (1999)
 JOURNAL MEDLINE 99277334
 PUBMED 10349831
 2 (bases 1 to 2725)
 Ou, X.M., Jafar-Nejad, H., Storring, J.M., Meng, J.H., Lemonde, S. and
 Albert, P.R.
 Novel dual repressor elements for neuronal cell-specific
 transcription of the rat 5-HT1A receptor gene
 J. Biol. Chem. 275 (11), 8161-8168 (2000)
 JOURNAL MEDLINE 20179926
 PUBMED 10713139
 3 (bases 1 to 2725)
 Storring, J.M. and Albert, P.R.
 Direct Submission

JOURNAL Submitted (16-DEC-1999) Neuroscience Res. Inst., University of
 Ottawa, 451 Smyth Road, Ottawa, ON K1H-8W5, Canada
 FEATURES
 Location/Qualifiers
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 1. 2725
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
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 1763..2725
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 /note="g protein-coupled receptor"
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 /db_xref="GI:6969400"
 /translation="MD"
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Query Match 4.6%; Score 139.6; DB 10; Length 2725;
 Best Local Similarity 57.9%; Pred. No. 1.2e-14;
 Matches 402; Conservative 0; Mismatches 249; Indels 43; Gaps 7;

QY 1054 CCTTATCCAAACACATCTCTCTGATTTGATATGATGCGCCCACTGATCTCTTTTGTAT 1113
 Db 218 CCATCTTCAGGTACACAGCCCTGGGTTAT-ATATTTCTGCCCACTGAGCTCTTTGGT 276
 QY 1114 GCTTGTGATTTGCTCTTTTGTGGGCTTGGAGATTCAGACTATGAAATTCAGAGCT 1173
 Db 277 GCTTTGATTTATCTCTTTCTTTGGTTTA-AGGTTTCAAAATATGATCCTCAAGCT 335
 QY 1174 CAGATTGACACATATTTAAGTTATTTGCAATCTGTAGTATCTGTTCATGTATCCA 1233
 Db 336 CAGATGTCAACACAAAGTAAGACAAATTCAGATTTGTACGGGCTCTGTGTGTCTTA 395
 QY 1234 GTGTCACTGCTTTGAGATTCAT-CCCTTCACTCAGGATGCAATTCAGATG 1288
 Db 396 GAATTTGGCTCTCTGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 455
 QY 1289 TATTAAGTAATGTTGTGTGTATGTTTACGTAGTGTCTTGAAGTCCATCTTTACCA 1348
 Db 456 TCTTAAG-CAGATCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 514
 QY 1349 ATGCTCAATGATTAATTTGTTTCTTGTAAAGAAACAGCTTAGAACACCTT 1408
 Db 515 ATCTCAGTTGGATGCTTTTGTTTTCCCAAAATACATGACTTAACAAATTCCT 574
 QY 1409 GTAAATCTTTATTTTCACTGATTTAATTTTCCAAATGTAAATCATTGGAAAAATGCA 1468
 Db 575 AAATGCTCTAATTTTCACTAATTAAGTCAATTC-----CTTATGAAAAAGGAA 622
 QY 1469 ATACTATTTGTTTCCCAAAAGTAATTTTATGAGTTCAGTTCCAAAGTTCAGTATGA 1528
 Db 623 ATATGCTCTTTTCCCAATTA-----ACATTTGATTTTATGACCAAACTGTGA 675
 QY 1529 CAGCAGAAACCAACAGAGTGAAGTGTAGCTTATTTAATATGCAATTCCTCAG 1588
 Db 676 CACACAGCAAAATAGCCGAAATGTGTGTCATTTCTTA----- 720
 QY 1589 TTGAACCTTTGATATACATATCTTCAAGCTTTTCCAAAGAGCTAAACATATATAG 1648
 Db 721 -TGAAGTTGTGATATGATGATCTTAAGCTTTCAAGAGAGCTTGAACATATGCGCAG 779
 QY 1649 CCGATATATTAAGTTCAAGCAAAAGAGGCGCACTTAATTTTAAAGAAATAG 1708
 Db 780 CTGTGTAACAAACCAAGAAAGAAAGAAAGAAAGAAATGATGAAGAAAAAT 839
 QY 1709 AAGAGCAAAATCTCAATCTACTCTGTCTTTA 1742
 Db 840 TTAAGTACATTTATGATTTATTTATTTA 873

RESULT 14
NMU33820 1256 bp DNA linear ROD 30-MAY-1996
LOCUS Mus musculus serotonin 1a receptor (Htr1a) gene, 5' flanking
DEFINITION sequence and partial cds.
ACCESSION U33820
VERSION U33820.1 GI:1335803
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 1256)
Parks, C.L. and Shenk, T.
TITLE The serotonin 1a receptor gene contains a TATA-less promoter that
responds to MAZ and Spl
J. Biol. Chem. 271 (8), 4417-4430 (1996)
MEDLINE 86224025
JOURNAL 8626793
REFERENCE 2 (bases 1 to 1256)
Parks, C.L. and Shenk, T.
AUTHORS Direct Submission
TITLE Submitted (12-AUG-1995) Christopher L. Parks, Molecular Biology,
Princeton University, Washington Road, Princeton, NJ 08544-1014,
USA
FEATURES
source Location/Qualifiers
1..1256
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/strain="C3H/Ar"
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511..1175
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1188..1256
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/product="serotonin 1a receptor"
/protein_id="AAC52572.1"
/db_xref="GI:1335804"
/translation="MDPSLGGQNNTTSLDHLGTG"
ORIGIN
Query Match 4.4%; Score 134.2; DB 10; Length 1256;
Best Local Similarity 64.7%; Pred. No. 1.2e-13;
Matches 288; Conservative 0; Mismatches 133; Indels 24; Gaps 5;
QY 2612 TTTTCCAAACCCAGTTTGTGTTGGAGGCGAGATTATTGTACAACCTTGCT 2671
Db 357 TTTTCCCTCTAGTTTAATAGTAAGAGCGGGGTTAGTAATTTAAACATGACT 416
QY 2672 GACCGGAGAGTCTGTGTGTGT---AAGTGAATTCTGAGTCTCTGTTGACAAAAGGA 2728
Db 417 GACTAGCAGATAGATAGATATATGAAGTGAATCTGAGTGTGTG-----GA 467
QY 2729 CTCGATGCAAGAGCGCTAGCTAGAGGAGAGAGGGGGGAGACCCAGAGAAAGAGGC 2788
Db 468 CTGGAATGTAAAGACTCTCGGCTACAGGAGAGAGGGGAGACCCAGAGAAAGAGGC 527
QY 2789 ACTCTCGGGGTTGGAGAGTATTAGAGAGGAGGCTTAGAGTGGAGAGGAGAGCCTG 2848
Db 528 ACTCGGAGCTAAGGAGATGTTGATGCGCGTGGGCTTTAACTGGAGAGAGGAGACTA 587
QY 2849 GCTTTGAGAGCACTACAGAGAGGATTAATAAGGAGAGTGAAGAGAGAGGAGACTG 2908
Db 588 GCTGTGTGAGCG--CACAAGAGACTTAAGAGAGAGGTGAGAGAGAGGAGAGACTG 645
QY 2909 AAAGGAGGCAAGTGGAGAGAGAGGAGAGGAGAGGAGAGGAGAGAGAGAA----- 2960

Db 646 AA--GGAAGCCAGTGGAGAGAAAGCCGGAGAGAAAGTGGAGAAAGAGAGCACTG 703
QY 2961 GAGAGAGGAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3020
Db 704 GAGAAAGCAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 763
QY 3021 TGACCGTGGAGATGGGGCTTCTCG 3045
Db 764 TGACCCGGAGAGATGGGGCTTCTCG 788
RESULT 15
LOCUS 166494/c 7218 bp DNA linear PAT 28-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION 166494
VERSION 166494.1 GI:2724471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 7218)
Dorner, F., Schefflinger, F. and Falkner, F. Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES
source Location/Qualifiers
1..7218
/organism="unknown"
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ORIGIN
Query Match 4.1%; Score 125.6; DB 6; Length 7218;
Best Local Similarity 2.1%; Pred. No. 2.8e-12;
Matches 8; Conservative 284; Mismatches 88; Indels 0; Gaps 0;
QY 2665 TTGGTCTGACCGGAGAGATCTGTGTGTGTAAGTCTGAGTCTGTTGACAAA 2724
Db 1441 TTGGTACRFR 1382
QY 2725 GAGACTGCAATGCAAGAGCGCTAGAGGAGAGAGAGGAGAGAGAGAGAGAG 2784
Db 1381 RRR 1322
QY 2785 AGGCACTCTCGGGGTTGGAGAGTATTAGAGAGGAGGTTAGAGTGGAGAGAG 2844
Db 1321 RRR 1262
QY 2845 CCGGCTTTCGAGAGCACTCACAGAGGATTAATAAGGAGAGTGAAGAGAGAG 2904
Db 1261 RRR 1202
QY 2905 ACTGAAAGGAGAGAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2964
Db 1201 RRR 1142
QY 2965 GAG 3024
Db 1141 RRR 1082
QY 3025 CGTGAAGATGGGCTTCTC 3044
Db 1081 RRRRRRRRRRRRRRRATCGC 1062
Search completed: April 10, 2004, 12:31:28
Job time: 1146 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 04:24:23 ; Search time 1068 seconds
(without alignments)
11889.488 Million cell updates/sec

Title: US-09-430-412a-1

Perfect score: 3045
Sequence: 1 atccatcataatccgtta.....gtggagagatgggctctcg 3045

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1959.2	64.3	3000	4	AAH88467
2	979.4	32.2	3001	4	AAH88468
3	747.8	24.6	1204	5	AAH75001
4	747.8	24.6	2722	5	AAH75003
5	742.4	24.4	839	3	AAH71827
6	742.4	24.4	839	3	AAH71824
7	742.4	24.4	839	3	AAH71830
8	522.4	17.2	2512	4	AAH88477
9	89.2	2.9	8056	7	ABT10246
10	86.6	2.9	8056	7	ABT10246
11	83.2	2.7	11745	6	ABK28332
12	82.4	2.7	6636	6	ABK28332
13	81.4	2.7	105325	6	ABK28332
14	81.2	2.7	8056	7	ABK28332
15	80.6	2.6	700	4	AAH93026
16	78.8	2.6	19787	5	ABK28394
17	77.8	2.5	19634	7	ABK28394
18	76.2	2.5	19634	7	ABK28394
19	75.2	2.5	8056	7	ABK28394
20	75.2	2.5	6317	6	ABK28394
21	75.2	2.5	6317	6	ABK28394
22	75.2	2.5	6317	6	ABK28394
23	75.2	2.5	7351	6	ABK28394

24	75.2	2.5	8222	7	ACF62816	ACF62816	Colon can
25	75.2	2.5	11222	9	ADBS4318	ADBS4318	Pretreat
26	74.8	2.5	5145	6	ABK28348	ABK28348	Human imm
27	74.8	2.5	5145	6	ABK28348	ABK28348	Human met
28	74.4	2.4	14919	4	AAH46506	AAH46506	Tumour su
29	74	2.4	665	3	AAH21986	AAH21986	Human apo
30	74	2.4	5689	4	AAH43584	AAH43584	Chemical
31	74	2.4	5689	4	AAH46426	AAH46426	Tumour su
32	74	2.4	5689	6	ABK28226	ABK28226	DNA trans
33	74	2.4	12237	7	ABK28358	ABK28358	Human imm
34	73.8	2.4	19634	7	ABK28358	ABK28358	Haematopo
35	73.6	2.4	4985	6	ABO75107	ABO75107	Anopheles
36	73.6	2.4	4985	6	ACF79270	ACF79270	Mosquito
37	73.6	2.4	8222	7	ACF62794	ACF62794	Colon can
38	73.6	2.4	11222	9	ADBS4190	ADBS4190	Pretreat
39	73.4	2.4	8170	6	ABK28258	ABK28258	DNA trans
40	73.2	2.4	18585	6	ABK28258	ABK28258	Human met
41	72.6	2.4	115218	7	ACA64845	ACA64845	Human HNR
42	72.2	2.4	6775	6	ABO67160	ABO67160	Human ang
43	72.2	2.4	32382	6	ABK28203	ABK28203	AMEV gen
44	72	2.4	2503	2	AAQ53480	AAQ53480	PYPX30 XY
45	72	2.4	5511	6	ABK3871	ABK3871	Human imm

ALIGNMENTS

RESULT 1	AAH88467/c	AAH88467 standard; DNA; 3000 BP.
ID	AAH88467;	
AC	AAH88467;	
XX		
DT	26-FEB-2002	(first entry)
XX		
DE	CNS disorder-related biallelic marker #1 from SMTA gene.	
XX		
KW	Single nucleotide polymorphism; SNP; biallelic marker; human; central nervous system disorder; CNS; serotonin receptor; ds.	
XX		
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	misc_feature	1501
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FT		/standard_name= "single nucleotide polymorphism"
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PN	W0200151659-A2.	
XX		
PD	19-JUL-2001.	
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PF	11-JAN-2001; 2001MO-18000116.	
XX		
PR	13-JAN-2000; 2000US-0175854P.	
XX		
PA	(GEST) GENSET.	
XX		
PI	Chu T, Blumenfeld M, Cohen D;	
XX		
DR	WPI; 2001-483085/52.	
XX		
XX		
FT	Isolated polynucleotides, useful for genotyping nucleic acids for biallelic markers for the diagnosis of depression, comprises central nervous system disorder related biallelic marker.	
PT		
XX		
PS	Claim 1; Page 335-336; 519pp; English.	
XX		
CC	The present invention relates to biallelic markers derived from human genes involved in central nervous system (CNS) disorders. The present sequence is one such biallelic marker derived from a human serotonin receptor gene. This marker has a single nucleotide polymorphism (SNP) and is useful in determining the genetic predisposition of individuals to CNS disorders, by identifying the nucleotides at a set of genetic markers in	

CC a biological sample, where the markers comprise at least one CNS disorder
CC related marker

Sequence 3000 BP; 783 A; 780 C; 665 G; 771 T; 0 U; 1 Other;

Query Match 64.3%; Score 1959.2; DB 4; Length 3000;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2018; Conservative 1; Mismatches 1; Indels 6; Gaps 6;

QY 1024 CTGAATATPAAAAAACAACAACAAACCTTATCCAAACACATGCTCTGATTTGA 1083
DB CTGAATATPAAAAAACAACAACAAACCTTATCCAAACACATGCTCTGATTTGA 2841
QY 1084 ATGCATGGCCCACTGGAATCTTTTGTATGCTTTGGATGCTTTGTTGGGCTT 1143
DB ATGCATGGCCCACTGGAATCTTTTGTATGCTTTGGATGCTTTGTTGGGCTT 2781
QY 1144 GAGAAATTCAGAGCTATGAAATTCAGAGCTGATTTGACAAATATTAATTAATTC 1203
DB GAGAAATTCAGAGCTATGAAATTCAGAGCTGATTTGACAAATATTAATTAATTC 2721
QY 1204 AATCTGTAGTAATCTGTTCATGTTATCCAGTGTCACTGCTTTGAGATTCATTCCTT 1263
DB AATCTGTAGTAATCTGTTCATGTTATCCAGTGTCACTGCTTTGAGATTCATTCCTT 2661
QY 1264 TCACCTCAGGCAATGCAATGAGATGATTAAGTAATGTTGTTGTTGTTTACTGTAG 1323
DB TCACCTCAGGCAATGCAATGAGATGATTAAGTAATGTTGTTGTTGTTTACTGTAG 2601
QY 1324 TTGCTTGAAGT -CATTCTTTACCAATGCTCAAAATGATTAATTTG -TTTCTGTGT 1381
DB TTGCTTGAAGTCCCATCTTTTACCAATGCTCAAAATGATTAATTTGTTTCTGTGT 2541
QY 1382 AAGGAAAGAGCTTGAACAACCCCTGTAATTAATCTTA -TTTGAATTTAATTT 1440
DB AAGGAAAGAGCTTGAACAACCCCTGTAATTAATCTTAATTTGAATTTAATTT 2481
QY 1441 CCMAATGTTAAATCAATTTGAAATATGCAATATCTATTCGTTTCCCAAAAGTAAAT 1500
DB CCMAATGTTAAATCAATTTGAAATATGCAATATCTATTCGTTTCCCAAAAGTAAAT 2421
QY 1501 TATGTCACTCCAAAGTTAGGTTATGACACAAACCAACAGGTGAAGTTAG 1560
DB TATGTCACTCCAAAGTTAGGTTATGACACAAACCAACAGGTGAAGTTAG 2361
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DB CCTAGCTTATTAATATGCAATTCAGTTAGAACTTGTAATGACATTAATCAAGCT 2301
QY 1621 TTGGAAGAGCTTAAACATATATATGCTGATATATATAGTTGACAGCAAGAGGCT 1680
DB TTGGAAGAGCTTAAACATATATATGCTGATATATATAGTTGACAGCAAGAGGCT 2241
QY 1681 ACTAAAAATTAATTTTAAAGAAATAGAAAGAGCAAAACTCAATACACTTCTCTT 1740
DB ACTAAAAATTAATTTTAAAGAAATAGAAAGAGCAAAACTCAATACACTTCTCTT 2181
QY 1741 TATAAATCTGCTCTCTCTTCTTAAAGTTGTTGTAATTCCTCAATACCTGCTCTCTT 1800
DB TATAAATCTGCTCTCTCTTCTTAAAGTTGTTGTAATTCCTCAATACCTGCTCTCTT 2121
QY 1801 GGCATTAAGGTTTCCAGATGCACTCTAAACATTTGCAAGAGTGGCAACATAAAC 1860
DB GGCATTAAGGTTTCCAGATGCACTCTAAACATTTGCAAGAGTGGCAACATAAAC 2063
QY 1861 CTCATTCCTTAGAATCTGCTCCAGTGTCTGAACCCAGTTCTGAGATTAAGAGGCTAGC 1920
DB CTCATTCCTTAGAATCTGCTCCAGTGTCTGAACCCAGTTCTGAGATTAAGAGGCTAGC 2003
QY 1921 CGGCTAGGCAACCGGATTCACCAAGTTTCCCGCAGAGGTTTGAAGGCTCTGTTAAATA 1980
DB CGGCTAGGCAACCGGATTCACCAAGTTTCCCGCAGAGGTTTGAAGGCTCTGTTAAATA 1943

QY 1981 GTGCAAAAGCCATGTGAATTCGAGGCTTCACTTGACACATATGCAAAATTTTCCA 2040
DB GTGCAAAAGCCATGTGAATTCGAGGCTTCACTTGACACATATGCAAAATTTTCCA 1883
QY 2041 TCCCTGAATTTACAGCAACAAAGCTATGAGAGTGGCAGTGCATGCACTGAATTAACAAGT 2100
DB TCCCTGAATTTACAGCAACAAAGCTATGAGAGTGGCAGTGCATGCACTGAATTAACAAGT 1823
QY 2101 TAGTAGATGAAAGAGTGTGTGTGTGTAGAAATATATATCACTGAGTGTGTGTCTT 2160
DB TAGTAGATGAAAGAGTGTGTGTGTGTGTAGAAATATATATCACTGAGTGTGTGTCTT 1763
QY 2161 CATTGCAAGATGAGT 2220
DB CATTGCAAGATGAGT 1703
QY 2221 TCTCTCCGCTCCCACTGTTAAAAAAGTCAAGGCAATTTCTCCCTGAGGAGT 2280
DB TCTCTCCGCTCCCACTGTTAAAAAAGTCAAGGCAATTTCTCCCTGAGGAGT 1643
QY 2281 AAGCTGGAATGTTAGATTAACGAGGTTACCTTTGTTGTTGTTGTTGTTGTTGTTGTTG 2340
DB AAGCTGGAATGTTAGATTAACGAGGTTACCTTTGTTGTTGTTGTTGTTGTTGTTGTTG 1583
QY 2341 GTTGTGTTTGAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
DB GTTGTGTTTGAAGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1523
QY 2401 ACGAGGTAGCTTTTAAAAAGAGACACATCGGCTTTCTTCATCAATATGACATAA 2460
DB ACGAGGTAGCTTTTAAAAAGAGACACATCGGCTTTCTTCATCAATATGACATAA 1463
QY 2461 TTGGAGACAGACCCAGGAGTGTACCTCCCATCAGGCTCCATGCTCTTCTTCT 2520
DB TTGGAGACAGACCCAGGAGTGTACCTCCCATCAGGCTCCATGCTCTTCTTCTTCT 1403
QY 2521 CATCTCTATTTGCACTGTGGATGTGACACAGATTTAAGATTTGACAGATATATAG 2580
DB CATCTCTATTTGCACTGTGGATGTGACACAGATTTAAGATTTGACAGATATATAG 1343
QY 2581 GCAAGAGTATGTTGAATTCCTCCCTCCCAAGTTTTCACACCCCAAGTTTTCGCGGCTG 2640
DB GCAAGAGTATGTTGAATTCCTCCCTCCCAAGTTTTCACACCCCAAGTTTTCGCGGCTG 1283
QY 1342 GCAAGAGTATGTTGAATTCCTCCCTCCCAAGTTTTCACACCCCAAGTTTTCGCGGCTG 1283
DB GCAAGAGTATGTTGAATTCCTCCCTCCCAAGTTTTCACACCCCAAGTTTTCGCGGCTG 2640
QY 2641 AAGCGAGATTTATTTGTTACCACTTGATCTGACCGGCA -GATCTGTGTGTGTAGT 2699
DB AAGCGAGATTTATTTGTTACCACTTGATCTGACCGGCA -GATCTGTGTGTGTAGT 1223
QY 1282 AAGCGAGATTTATTTGTTACCACTTGATCTGACCGGCA -GATCTGTGTGTAGT 1223
DB AAGCGAGATTTATTTGTTACCACTTGATCTGACCGGCA -GATCTGTGTGTAGT 1223
QY 2700 AGTTCTGAGTCTGTGTGACAAAGAGACTCGAATGCAAAAGCGTGAAGTGAAGAG 2759
DB AGTTCTGAGTCTGTGTGACAAAGAGACTCGAATGCAAAAGCGTGAAGTGAAGAG 1163
QY 1222 AGTTCTGAGTCTGTGTGACAAAGAGACTCGAATGCAAAAGCGTGAAGTGAAGAG 1163
DB AGTTCTGAGTCTGTGTGACAAAGAGACTCGAATGCAAAAGCGTGAAGTGAAGAG 2819
QY 2760 AAGAGGCGGAGGACCAAGAGAAAGAGCACTCTCGGCTTGGGAAATTAAGAGG 2819
DB AAGAGGCGGAGGACCAAGAGAAAGAGCACTCTCGGCTTGGGAAATTAAGAGG 1103
QY 1162 AAGAGGCGGAGGACCAAGAGAAAGAGCACTCTCGGCTTGGGAAATTAAGAGG 1103
DB AAGAGGCGGAGGACCAAGAGAAAGAGCACTCTCGGCTTGGGAAATTAAGAGG 2879
QY 2820 GAGGCTTAAAGTGGAGAGAGAGAGCTTGCTTTCGAAGGATTCACAGAGGATTAATA 2879
DB GAGGCTTAAAGTGGAGAGAGAGAGCTTGCTTTCGAAGGATTCACAGAGGATTAATA 1043
QY 1102 GAGGCTTAAAGTGGAGAGAGAGAGCTTGCTTTCGAAGGATTCACAGAGGATTAATA 1043
DB GAGGCTTAAAGTGGAGAGAGAGAGCTTGCTTTCGAAGGATTCACAGAGGATTAATA 2880
QY 2880 AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAGAG 2939
DB AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAGAG 983
QY 1042 AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 983
DB AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 2940
QY 2940 AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 2939
DB AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 983
QY 982 AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 923
DB AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 3000
QY 3000 AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 3045
DB AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 922
QY 922 AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG 877
DB AAGGAAATGAGAGAGAGAGAGAGCTGAAAGGAAAGCAGGATGAGAGAGAGAGAG

ID	AAH88468	standard; DNA; 3001 BP.
XX	AAH88468;	
XX	26-FEB-2002	(first entry)
XX	CNS disorder-related biallelic marker #2 from 5HT1A gene.	
XX	Single nucleotide polymorphism; SNP; biallelic marker; human;	
XX	central nervous system disorder; CNS; serotonin receptor; ds.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	misc_feature	1501
XX	FT	/*tag= a
XX	FT	/standard_name= "single nucleotide polymorphism"
XX	W0200151659-A2.	
XX	19-JUL-2001.	
XX	11-JAN-2001; 2001WO-IB000116.	
XX	13-JAN-2000; 2000US-0175854P.	
XX	(GEST) GENSET.	
XX	Chu T, Blumenfeld M, Cohen D;	
XX	WPI; 2001-483085/52.	
XX	Isolated polymorphisms, useful for genotyping nucleic acids for	
XX	biallelic markers for the diagnosis of depression, comprises central	
XX	nervous system disorder related biallelic marker.	
XX	Claim 1; Page 337; 519pp; English.	
XX	The present invention relates to biallelic markers derived from human	
XX	genes involved in central nervous system (CNS) disorders. The present	
XX	sequence is one such biallelic marker derived from a human serotonin	
XX	receptor gene. This marker has a single nucleotide polymorphism (SNP) and	
XX	is useful in determining the genetic predisposition of individuals to CNS	
XX	disorders, by identifying the nucleotides at a set of genetic markers in	
XX	a biological sample, where the markers comprise at least one CNS disorder	
XX	related marker	
XX	Sequence 3001 BP; 654 A; 799 C; 856 G; 678 T; 0 U; 14 Other;	
XX	Query Match	32.2%; Score 979.4; DB 4; Length 3001;
XX	Best Local Similarity	98.7%; Pred. No. 7.2e-176;
XX	Matches 1005; Conservative	0; Mismatches 11; Indels 2; Gaps 2;
XX	2029	AAATATTTCATCCCTGAAATTATAGCACAAAGCTATGGAGAGTGGACGTGCACGTG 2088
XX	9	AAATATTTCATCCCTGAAATTATAGCACAAAGCTATGGAGAGTGGACGTGCACGTG 68
XX	2089	AAATTCACAGTGTAGTAGTAGGAAAAGTGTGTGTGTATTAGAAATATATATACACTG 2144
XX	69	AAATTCACAGTGTAGTAGTAGGAAAAGTGTGTGTGTATTAGAAATATATATACACTG 128
XX	2149	AGTTTGTCTTCATTTGAGATGAGTGTGTATACCTCCCTGTCCTTTACACAGTCT 2200
XX	129	AGTTTGTCTTCATTTGAGATGAGTGTGTATACCTCCCTGTCCTTTACACAGTCT 188
XX	2209	TTATATATTGTTCTCTCCCGGTTCCCAAGCTTAAAAAAAAGTCACAGGCATATCT 2266
XX	189	TTATATATTGTTCTCTCCCGGTTCCCAAGCTTAAAAAAAAGTCACAGGCATATCT 248
XX	2269	CCCTGAGGAGTAAGCTGAGCTGTATATATGATTAACGAGATCCGTTTGTGTGTGTG 2322

Db	249	CCCTGAGGGAACTAAGGCTGAGCTGTTAGATGATTAACGAAAGGTACCGCTTTGTTGTTG 308
Qy	2329	TTCGTCGTTGTCGTTTGTTGTTTGGAGACGGAGCTCCTGCTCTGTCGCCAGGCTGGAGTGC 2388
Db	309	TGCGTCGNTGTCGTTTGTTGTTTGGAGACGGAGTCTCGTCTGTGCGCCAGGCTGGAGTGC 368
Qy	2389	AATGGCGGAGAAACGAGAGTACGCTTTTAAAAACGAAACACACTCGGTCTTCTTCATC 2448
Db	369	AATGGCGGAGAAACGAGAGTACGCTTTTAAAAACGAAACACACTCGGTCTTCTTCATC 428
Qy	2449	AATTAGCAATATTGGGAGACTGACCCAGGACTGTTACCTTTCCATTCAAGCTCCCAT 2508
Db	429	AATTAGCAATATTGGGAGACTGACCCAGGACTGTTACCTTTCCATTCAAGCTCCCAT 488
Qy	2509	GCTTCCTTTTCTCAATCCTCAATGCGAATCGGAGATGCTGACACGATTTAAGATTGAC 2568
Db	489	GCTTCCTTTTCTCAATCCTCAATGCGAATCGGAGATGCTGACACGATTTAAGATTGAC 548
Qy	2569	AGATTAATATGAGGCAAGAGTAGTTGGAATTCCTCCCAAGTTTTCACACCCCAAGTT 2628
Db	549	AGATTAATATGAGGCAAGAGTAGTTGGAATTCCTCCCAAGTTTTCACACCCCAAGTT 608
Qy	2629	TTGCTGGGTTTGGAGCGGAGTTTATTGTTTCAACCTTGCTGACCGGCA-GGATCTGG 2688
Db	609	TTGCTGGGTTTGGAGCGGAGTTTATTGTTTCAACCTTGCTGACCGGCAAGGACTGG 668
Qy	2688	TGTGTGTATGAGATTCTGAGTCTCTGTGTGCAAAAAAGAGACTCGAATGCAAAAGACTG 2748
Db	669	TGTGTGTATGAGATTCTGAGTCTCTGTGTGCAAAAAAGAGACTCGAATGCAAAAGACTG 728
Qy	2748	AGCTTAGAGGAGAGAGAGGCGGGGACCCAGAGAAAGAGCACTCTCTGGGGTTGGGAA 2808
Db	729	AGCTTAGAGGAGAGAGAGGCGGGGACCCAGAGAAAGAGCACTCTCTGGGGTTGGGAA 788
Qy	2808	GTATTAGAGGAGAGGTTAGTGTGAGGAGGAGAGGCTGCTTCCAGAGCACTCACA 2868
Db	789	GTATTAGAGGAGAGGTTAGTGTGAGGAGGAGAGGAGG-CTGCTTTCGAAAGCACTCACA 848
Qy	2868	GAGGGATTAAATGAAGGAAAGTGAAGGAGAGAGGAGACTGAAGAGGAAAGGCAAGCTGGGG 2928
Db	848	GAGGGATTAAATGAAGGAGAGTGAAGGAGAGAGGAGAGGAGACTGAAGAGGAAAGGCAAGCTGGGG 908
Qy	2928	AGAAAGGGGAGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 2988
Db	908	AGAAAGGGGAGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 968
Qy	2988	AAGGAAGGAATTAAGGAGAGAGAGGAGTCAAGAGTGAACCGTGAGAGATGGGCTTCTCG 3048
Db	968	AAGGAAGGAATTAAGGAGAGAGAGGAGTCAAGAGTGAACCGTGAGAGATGGGCTTCTCG 1028
RESULT 3		
AAAF75001 standard; DNA; 1204 BP.		
XX	AAAF75001;	
AC	AAF75001;	
XX	AAF75001;	
DT	08-MAY-2001 (first entry)	
XX	Part of HTR1A gene #1.	
DE		
XX	5-hydroxy tryptamine receptor 1A; HTR1A; polymorphism; Tourette's;	
KW	neuropsychiatric; de.	
KW		
XX	Homo sapiens.	
OS		
XX	WO200110884-A1.	
XX	15-FEB-2001.	
PD		
XX	01-AUG-2000; 2000WO-USO40519.	
PF		
XX	06-AUG-1999; 99US-0147711P.	

XX (GENA-) GENAISSANCE PHARM INC.
 XX Denton RR, Klielem SE, Nandabalan K, Stephens JC;
 XX WPI; 2001-191514/19.
 XX
 PT New 5-hydroxy tryptamine receptor 1A gene variants for studying
 PT expression and biological function of the gene and for developing drugs
 PT targeting 5-hydroxy tryptamine receptor 1A protein.
 XX
 PS Disclosure; Fig 1; 64pp; English.
 XX
 CC The present invention relates to 5-hydroxy tryptamine receptor 1A (HTR1A)
 CC gene. HTR1A-encoding polynucleotides containing one or more of the novel
 CC polymorphic sites are useful in studying the expression and biological
 CC function of HTR1A, as well as in developing drugs targeting this protein.
 CC In addition, information on the combinations of polymorphisms in the
 CC HTR1A gene may have diagnostic and forensic applications. A polymorphic
 CC variant of HTR1A is useful in studying the effect of the variation on the
 CC biological activity of HTR1A as well as studying the binding affinity of
 CC candidate drugs targeting HTR1A for the treatment of neuropsychiatric
 CC diseases and Tourette's syndrome
 XX
 SQ Sequence 1204 BP; 283 A; 266 C; 394 G; 261 T; 0 U; 0 Other;
 Query Match 24.6%; Score 747.8; DB 5; Length 1204;
 Best Local Similarity 98.9%; Pred. No. 4,3e-132;
 Matches 774; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
 QY 2264 ATTCTCCCTGAGGAGTAAGCTGAGCTGTAGATGATTAACGAGATACCGTTTGTGT 2323
 DB 1 ATTCTCCCTGAGGAGTAAGCTGAGCTGTAGATGATTAACGAGATACCGTTTGTGT 60
 QY 2324 TGTGTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2383
 DB 61 TGTGTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120
 QY 2384 AGTGCATGCGCGAGAGACGAGAGTACTTTTAAAGACAGACACTCGTCTTCTT 2443
 DB 121 AGTGCATGCGCGAGAGACGAGAGTACTTTTAAAGACAGACACTCGTCTTCTT 180
 QY 2444 CCATCAATTAGCATTAATTGGAGACTGACCCAGAGCTGTTCACTTCCATTAGGCTC 2503
 DB 181 CCATCAATTAGCATTAATTGGAGACTGACCCAGAGCTGTTCACTTCCATTAGGCTC 240
 QY 2504 CCATGCTCTCTTTCTCATCTCTATGCGACTGCGGAGTGTGACAGATTAGAT 2563
 DB 241 CCTGCTCTCTTTCTCATCTCTATGCGACTGCGGAGTGTGACAGATTAGAT 300
 QY 2564 TTGGCAGATTAATATGAGGAGAGAGTGAATTCCTCCCGCAAGTTTTCACACC 2623
 DB 301 TTGGCAGATTAATATGAGGAGAGAGTGAATTCCTCCCGCAAGTTTTCACACC 360
 QY 2624 CAGTTTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2682
 DB 361 CAGTTTGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 420
 QY 2683 TCTGTGTGTGTAAGTGAATCTGACTCTCTGTGTCAGAAAAGAGACTGATGCAAGA 2742
 DB 421 CTTGCTGTGTGTAAGTGAATCTGACTCTCTGTGTCAGAAAAGAGACTGATGCAAGA 480
 QY 2743 CGCTGAGTGAAGGAGAGAGGCGGAGACCCAGAGAAAGAGCACTCTCCGGGTTG 2802
 DB 481 CGCTGAGTGAAGGAGAGAGGCGGAGACCCAGAGAAAGAGCACTCTCCGGGTTG 540
 QY 2803 GGGAACTATTAGAGGAGAGGTTAGAGTGGAGGAGAGAGAGCTGCTTTGAGAGCAG 2862
 DB 541 GGGAACTATTAGAGGAGAGGTTAGAGTGGAGGAGAGAGAGCTGCTTTGAGAGCAG 599
 QY 2863 TCACAGAGGATTAATAAGGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2922
 DB 600 TCACAGAGGATTAATAAGGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 659

QY 2923 TGGGAGAGAGGAG 2982
 DB 660 TGGGAGAGAGGAG 719
 QY 2983 GAGGAG 3042
 DB 720 GAGGAG 779
 QY 3043 TCG 3045
 DB 780 TCG 782
 RESULT 4
 AAF75003
 ID AAF75003 standard; DNA; 2722 BP.
 XX
 AC AAF75003;
 XX
 DT 08-MAY-2001 (first entry)
 DE
 DE Part of HTR1A gene #3.
 XX
 KM 5-hydroxy tryptamine receptor 1A; HTR1A; polymorphism; Tourette's;
 KM neuropsychiatric; ds.
 OS Homo sapiens.
 PN W0200110884-A1.
 PD 15-FEB-2001.
 PF 01-AUG-2000; 2000MO-US040519.
 PR 06-AUG-1999; 99US-0147711P.
 PA (GENA-) GENAISSANCE PHARM INC.
 PI Denton RR, Klielem SE, Nandabalan K, Stephens JC;
 DR WPI; 2001-191514/19.
 XX
 PT New 5-hydroxy tryptamine receptor 1A gene variants for studying
 PT expression and biological function of the gene and for developing drugs
 PT targeting 5-hydroxy tryptamine receptor 1A protein.
 XX
 PS Claim 1; Fig 3; 64pp; English.
 XX
 CC The present invention relates to 5-hydroxy tryptamine receptor 1A (HTR1A)
 CC gene. HTR1A-encoding polynucleotides containing one or more of the novel
 CC polymorphic sites are useful in studying the expression and biological
 CC function of HTR1A, as well as in developing drugs targeting this protein.
 CC In addition, information on the combinations of polymorphisms in the
 CC HTR1A gene may have diagnostic and forensic applications. A polymorphic
 CC variant of HTR1A is useful in studying the effect of the variation on the
 CC biological activity of HTR1A as well as studying the binding affinity of
 CC candidate drugs targeting HTR1A for the treatment of neuropsychiatric
 CC diseases and Tourette's syndrome
 XX
 SQ Sequence 2722 BP; 582 A; 743 C; 811 G; 586 T; 0 U; 0 Other;
 Query Match 24.6%; Score 747.8; DB 5; Length 2722;
 Best Local Similarity 98.9%; Pred. No. 5e-132; 7; Indels 2; Gaps 2;
 Matches 774; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
 QY 2264 ATTCTCCCTGAGGAGTAAGCTGAGCTGTAGATGATTAACGAGATACCGTTTGTGT 2323
 DB 1 ATTCTCCCTGAGGAGTAAGCTGAGCTGTAGATGATTAACGAGATACCGTTTGTGT 60
 QY 2324 TGTGTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2383
 DB 61 TGTGTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 120

QY 2384 AGTCAATGGCGGAGAAAGGAGTAACTTTTAAAAAGAAAGACACTGGTCTTCT 2443
 Db 121 AGTCAATGGCGGAGAAAGGAGTAACTTTTAAAAAGAAAGACACTGGTCTTCT 180
 QY 2444 CCATCAATTAACAAATTAATGGAGACTGACCCAGAGACTGCTTCCACTTCCACTTACAGCTC 2503
 Db 181 CCATCAATTAACAAATTAATGGAGACTGACCCAGAGACTGCTTCCACTTCCACTTACAGCTC 240
 QY 2504 CCTATGCTTCCCTTTCTCATCTCTCATCTGCACTCTGGAGTGTGACAGATTTAAGAT 2563
 Db 241 CCTATGCTTCCCTTTCTCATCTCTCATCTGCACTCTGGAGTGTGACAGATTTAAGAT 300
 QY 2564 TTGGCAGTAATTAATGAAGGAGAGAGTAAATTCCTTCCCAAGTTTTCACACC 2623
 Db 301 TTGGCAGTAATTAATGAAGGAGAGAGTAAATTCCTTCCCAAGTTTTCACACC 360
 QY 2624 CAGTTTCTGGGTTGAGGCGGAGATTATTTGTAACACCTTGTCTGACCGGCA-GGA 2682
 Db 361 CAGTTTCTGGGTTGAGGCGGAGATTATTTGTAACACCTTGTCTGACCGGCAAGGA 420
 QY 2683 TCTGGTGTGTAAAGTAACTCTGAGTCTCTGTTGACAAAAGAGACTCGAATGCAAGA 2742
 Db 421 CCTGGTGTGTAAAGTAACTCTGAGTCTCTGTTGACAAAAGAGACTCGAATGCAAGA 480
 QY 2743 CGTGAAGCTAAGAGAGAGAGGCGCGGAGACCCAGAGAAAGAGCACTCTCGGGGTTG 2802
 Db 481 CGTGAAGCTAAGAGAGAGGCGCGGAGACCCAGAGAAAGAGCACTCTCGGGGTTG 540
 QY 2803 GGAAGATTAATGAAGGAGGAGGTTAGAGTGGAGGAGAGAGCCTTGCTTCAGAGGAC 2862
 Db 541 GGAAGATTAATGAAGGAGGAGGTTAGAGTGGAGGAGAGAGAG-CCTGCTTCAGAGGAC 599
 QY 2863 TCACAGAGGATTAATTAAGGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2922
 Db 600 TCACAGAGGATTAATTAAGGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
 QY 2923 TGGGAGAGAGGAG 2982
 Db 660 TGGGAGAGAGGAG 719
 QY 2983 GAGGAG 3042
 Db 720 GAGGAG 779
 QY 3043 TCG 3045
 Db 780 TCG 782
 RESULT 5
 AAC71827
 ID AAC71827 standard; DNA; 839 BP.
 XX
 AC AAC71827;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Single nucleotide polymorphism containing sequence #552.
 XX
 KW Single nucleotide polymorphism; SNP; human; genetic disease;
 KW disease susceptibility; cardiovascular system; endocrine system;
 KW neurological system; forensic testing; paternity testing; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200058519-A2.
 XX
 BD 05-OCT-2000.
 XX
 PF 30-MAR-2000; 2000WO-US008440.
 XX
 PR 31-MAR-1999; 99US-0127248P.

XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 PA (AFY-) AFFYMETRIX INC.
 XX
 PI Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
 PI Lipshutz RJ, Patil N, Sklar P;
 DR WPI; 2000-611722/58.
 XX
 PT Nucleic acid selected from one of 106 genes comprising single nucleotide
 PT polymorphisms, allele-specific oligonucleotides to the genes are useful
 PT for phenotypic correlations, forensics, paternity testing, medicine and
 PT genetic analysis.
 XX
 PS Claim 1, Fig 5; 214pp; English.
 XX
 CC The present invention is concerned with a number of human single
 CC nucleotide polymorphisms (SNPs) which the inventors identified in human
 CC genes. These SNPs can be used in disease diagnosis and prediction of an
 CC individual's susceptibility to disease, in forensic and paternity testing
 CC and in genetic mapping. In particular, the SNPs of the invention can be
 CC used to diagnose susceptibility to diseases of the cardiovascular,
 CC endocrine and neurological systems, such as coronary artery disease,
 CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
 CC diseases. Note: The degenerate codon within the sequence represents the
 CC position of an SNP, for example the letter S represents a polymorphism
 CC where the nucleotide may be C or G
 CC
 SQ Sequence 839 BP; 212 A; 148 C; 287 G; 191 T; 0 U; 1 Other;
 Query Match 24.4%; Score 742.4; DB 3; Length 839;
 Best Local Similarity 98.7%; Pred. No. 4.2e-131;
 Matches 768; Conservative 1; Mismatches 7; Indels 2; Gaps 2;
 QY 2269 CCTGAGGAGTAAGGCTGAGCTTGAATGATTAACGAGAGTACGTTTGTGTTGTTG 2328
 Db 1 CCTGAGGAGTAAGGCTGAGCTTGAATGATTAACGAGAGTACGTTTGTGTTGTTG 60
 QY 2329 TCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2388
 Db 61 TCGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
 QY 2389 AATGGCGGAGAAAGGAGGTAAGCTTTTAAAAAGAGAGACACTGCTTCTTCATC 2448
 Db 121 AATGGCGGAGAAAGGAGGTAAGCTTTTAAAAAGAGAGACACTGCTTCTTCATC 180
 QY 2449 AATTGCAATTAATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2508
 Db 181 AATTGCAATTAATTTGGAG 240
 QY 2509 GCTTCTTCTTCATCTCTATTTGTCACCTGTTGAGTGTGACAGATTTAAGATTTGGC 2568
 Db 241 GCTTCTTCTTCATCTCTATTTGTCACCTGTTGAGTGTGACAGATTTAAGATTTGGC 300
 QY 2569 AGATTAATTAAG 2628
 Db 301 AGATTAATTAAG 360
 QY 2629 TTGCTGGTTGAGGCGGAGATTATTTGTTACAACCTTGTCTGACCGGCA-GGATCTGG 2687
 Db 361 TTGCTGGTTGAGGCGGAGATTATTTGTTACAACCTTGTCTGACCGGCAAGGACTGG 420
 QY 2688 TGTGTGAAGTGAATTTCTGAGTCTCTGTTGACAAAAGAGACTCGAATGCAAGAGCTG 2747
 Db 421 TGTGTGAAGTGAATTTCTGAGTCTCTGTTGACAAAAGAGACTCGAATGCAAGAGCTG 480
 QY 2748 AGCTAGAGGAGAGAGAGGCGGAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2807
 Db 481 AGCTAGAGGAGAGAGAGGCGGAGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 2808 GTAATTAGAGGAGAGAGGTTAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2867
 Db 541 GTAATTAGAGGAGAGAGGTTAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599


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PR 31-MAR-1999; 99US-0127248P.
XX
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
XX Alshuler D, Gargali M, Daley GO, Ireland JS, Lander ES;
PI Lippshutz RJ, Patil N, Sklar P;
XX
XX WPI; 2000-611722/58.
XX
XX Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
XX Claim 1; Fig 5; 214pp; English.
XX
XX The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases. Note: The degenerate codon within the sequence represents the
CC position of an SNP, for example the letter S represents a polymorphism
CC where the nucleotide may be C or G
XX
XX Sequence 839 BP; 212 A; 148 C; 287 G; 191 T; 0 U; 1 Other;
SQ
Query Match 24.4%; Score 742.4; DB 3; Length 839;
Best Local Similarity 98.7%; Pred. No. 4.2e-131;
Matches 768; Conservative 1; Mismatches 7; Indels 2; Gaps 2;
QY 2269 CCTGAGGAGTAAAGCTGAGCTGATGATGATACGAGAGTACCGTTTGTGTTG 2328
DB 1 CCTGAGGAGTAAAGCTGAGCTGATGATGATGATGATGATGATGATGATGATG 60
QY 2329 TCGTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2388
DB 61 TCGTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
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XX Single nucleotide polymorphism; SNP; biallelic marker; human;
XX central nervous system disorder; CNS; serotonin receptor; ds.
XX Homo sapiens.
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FT /standard_name= "single nucleotide polymorphism"
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XX 19-JUL-2001.
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XX 11-JAN-2001; 2001WO-1B000116.
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XX 13-JAN-2000; 2000US-0175854P.
XX
XX (GENSER ) GENSER.
XX
XX Chu T, Blumenfeld M, Cohen D;
PI
XX
XX WPI; 2001-483085/52.
XX
XX Isolated polymucleotides, useful for genotyping nucleic acids for
PT biallelic markers for the diagnosis of depression, comprises central
PT nervous system disorder related biallelic marker.
XX
XX Claim 1; Page 344-345; 519pp; English.
XX
XX The present invention relates to biallelic markers derived from human
CC genes involved in central nervous system (CNS) disorders. The present
CC sequence is one such biallelic marker derived from a human serotonin
CC receptor gene. This marker has a single nucleotide polymorphism (SNP) and
CC is useful in determining the genetic predisposition of individuals to CNS
CC disorders, by identifying the nucleotides at a set of genetic markers in
CC a biological sample, where the markers comprise at least one CNS disorder
CC related marker
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 12:31:35 ; Search time 8774 Seconds
(without alignments)
12211.276 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 75154660

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Listing first 45 summaries

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ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Albert Paul, and Lemonde, Sylvie
TITLE OF INVENTION: Mutations in the 5' region of the human 5-HT1A gene,
associated proteins of the 5' region and a diagnostic
TITLE OF INVENTION: test for major depression and related mental illnesses
FILE REFERENCE: 881014US1
CURRENT APPLICATION NUMBER: US/09/430, 412A
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,375
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3045
TYPE: DNA
ORGANISM: human

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SEQ ID NO: 83506
LENGTH: 13269
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ORGANISM: Homo sapiens
US-60-466-412-83506

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Best Local Similarity 97.4%; Pred. No. 0;
Matches 2984; Conservative 5; Mismatches 45; Indels 29; Gaps 20;

QY 1 ATCATCATATATACCGCTTAATAAGCTTCTTTCTTAGCTTAACCTTAGAGCCCTTGA 60
DB 2554 ATCATCATATATACCGCTTAATAAGCTTCTTTCTTAGCTTAACCTTAGAGCCCTTGA 2613
QY 61 AGATAAGAGCTCATCTCTTTA--CAGAGCTTGGTTGACAGCTTTACTTAAAGAAATA 118
DB 2614 AGATAAGAGCTCATCTCTTTAAGAGAGCTTGGTTGACAGCTTTACTTAAAGAAATA 2673
QY 119 TTGGTATCTCTGATCTTTTAAGAGTTAAACATAGAGAAATGGCTAAGTGAATG 178
DB 2674 TTGGTATCTCTGATCTTTTAAGAGTTAAACATAGAGAAATGGCTAAGTGAATGAA-G 2732
QY 179 AAAGCAATATCATCTTGCATATATCATTTATATATATACAGATTTATAGTTT-AA 237
DB 2733 AAAGCAATATCATCTTGCATATATCATTTATATATATACAGATTTATAGTTTAA 2792
QY 238 AAGTTAAACATAATATCTATATATATATATATATATATATATATATATATATAT 297
DB 2793 AAGTTAAACATAAT 2851
QY 298 GAATTAATCTGATCT 357
DB 2852 ATA--CTTCAATCT 2907
QY 358 TTAAATGTAGAAATTAATAATGTGTAATATATATATATATATATATATATATATAT 417
DB 2908 TTAAATGTAGAAATTAATAATGTGTAATATATATATATATATATATATATATATAT 2967
QY 418 GAATTAATCTGATCT 477
DB 2968 GAATTAATCTGATCT 3026
QY 478 AATAACAAATGCTATACCTCAGGAATATATATATATATATATATATATATATATAT 537
DB 3027 AATAACAAATGCTATACCTCAGGAATATATATATATATATATATATATATATATAT 3086
QY 538 TGATGAGAAAAATTAATAATGTGTAATATATATATATATATATATATATATATATAT 596
DB 3087 TGATGAGAAAAATTAATAATGTGTAATATATATATATATATATATATATATATATAT 3146
QY 597 GAATTAATCTGATCT 656
DB 3147 GAATTAATCTGATCT 3206
QY 657 GACACAAATCTTATATATGTCTTGATATGACATATATATATATATATATATATATAT 716
DB 3207 GACACAAATCTTATATATGTCTTGATATGACATATATATATATATATATATATATAT 3266
QY 717 CTATATTAATCTTGTATATAGTCAACTATATATATATATATATATATATATATATAT 776
DB 3267 CTATATTAATCTTGTATATAGTCAACTATATATATATATATATATATATATATATAT 3326
QY 777 AGCCTTTAAATATTTTCCATATATATATATATATATATATATATATATATATATAT 836
DB 3327 AG-CTTTAAATATTTTCCATATATATATATATATATATATATATATATATATATAT 3384
QY 837 ATTAATCTCTGATTTGTGAGAGACTTTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 896

DB 3385 ATATAGTCTGATATTTGTGAAGAGCTTTAGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3444
QY 897 -AAAGACTTCTTCAAGCTCTGTAAACAGATTACCATGATATATCTCTCTCTTTC 955
DB 3445 AAAAGACTTCTTCAAGCTCTGTAAACAGACTTACCATGATATATCTCTCTCTTTC 3504
QY 956 ATGCC---ATGATCATCAAGATGAGGCTCAAGTGTGGCAGTGGC-AATGATGAGT 1010
DB 3505 AATGCCAATCATCAAGATGAGGCTCAAGTGTGGCAGTGGC-AATGATGAGT 3564
QY 1011 GGGACTGTGCC---AGCTGACTATATAAAAAAAAAAAAAACAACAAACCTTATCCAACA 1066
DB 3565 GGGACTGTGCCAGACTGTAAATATAAAAAAAAAAAAAACAACAAACCTTATCCAACA 3624
QY 1067 CACTGTCTGTATGTATATGATATGAGTGGCCCACTGGATTTCTTTGAGCTTGGTGAATG 1126
DB 3625 CACTGTCTGTATGTATATGATATGAGTGGCCCACTGGATTTCTTTGAGCTTGGTGAATG 3684
QY 1127 CTCTTTGTGGGCTTGGAGAAATTCAGAGCTATGAATTCAGAGCTCAGATTTGAACAC 1186
DB 3685 CTCTTTGTGGGCTTGGAGAAATTCAGAGCTATGAATTCAGAGCTCAGATTTGAACAC 3744
QY 1187 AATATTAAGATTAATGCAATCTGTATGATATCTGTATATATCAAGTCAACTGCTT 1246
DB 3745 AATATTAAGATTAATGCAATCTGTATGATATCTGTATATATCAAGTCAACTGCTT 3804
QY 1247 TTGAGATATGCAATCTTCACTCAGGAGATCAATCAAGATATGAAGTGAAGTGTGTG 1306
DB 3805 TTGAGATATGCAATCTTCACTCAGGAGATCAATCAAGATATGAAGTGAAGTGTGTG 3864
QY 1307 TGTATGTATCTGATGTGCTTGAAGT--CAATCTTTTACCAATGCTCAATGCTATTA 1365
DB 3865 TGTATGTATCTGATGTGCTTGAAGT--CAATCTTTTACCAATGCTCAATGCTATTA 3924
QY 1366 AATTTG--TTTCTGTATTAAGAAACAGCTTAGAACAACCTGTGAATCTTA--TT 1423
DB 3925 AATTTGTTTCTGTATTAAGAAACAGCTTAGAACAACCTGTGAATCTTA--TT 3984
QY 1424 TCAGATATTAACATTTCCAAATGTAAATCATTTGGAATAATGCAATATATGCTTCT 1483
DB 3985 TCAGATATTAACATTTCCAAATGTAAATCATTTGGAATAATGCAATATATGCTTCT 4044
QY 1484 CCAACAAAGGTAATTTATATGCTCAAGTCCAAAGTCAAGTTATGACAGCAACAAACAC 1543
DB 4045 CCAACAAAGGTAATTTATATGCTCAAGTCCAAAGTCAAGTTATGACAGCAACAAACAC 4104
QY 1544 ACAGGTGAAGTGTAGCTTATATTAATATGCAATCCAGTGAAGTGTGAAT 1603
DB 4105 ACAGGTGAAGTGTAGCTTATATTAATATGCAATCCAGTGAAGTGTGAAT 4164
QY 1604 GACAGATATCTCAGGCTTTGGAAGAAAGCTAAACATATATATAGGCTGATATATAGT 1663
DB 4165 GACAGATATCTCAGGCTTTGGAAGAAAGCTAAACATATATATAGGCTGATATATAGT 4224
QY 1664 TCAGAGCAAAAGGAGGCACTTAATAATTTTAAAGAAATGAGAGGAGCAAAACCTC 1723
DB 4225 TCAGAGCAAAAGGAGGCACTTAATAATTTTAAAGAAATGAGAGGAGCAAAACCTC 4284
QY 1724 AATACTACCTTGTCTTTAATACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1783
DB 4285 AATACTACCTTGTCTTTAATACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4344
QY 1784 ATACTTGTCTTATTTTGTGAGATATAGGTTTCCAGATGCACTTAAACATTTGCCAGAA 1843
DB 4345 ATACTTGTCTTATTTTGTGAGATATAGGTTTCCAGATGCACTTAAACATTTGCCAGAA 4403
QY 1844 GGTGGCAACATAAAACCTCATGTCTTGAACATGCTCCAGAGTCTGAACCCAGTTTCTGA 1903
DB 4404 GGTGGC-ACATTAACCTCATGTCTTGAACATGCTCCAGAGTCTGAACCCAGTTTCTGA 4462
QY 1904 GATTAAAGAGGCTAGCGGCTTAGCGAACCGGATTCACCAAGTTTCCCCAGAGTTT 1963
DB 4463 GATTAAAGAGGCTAGCGGCTTAGCGAACCGGATTCACCAAGTTTCCCCAGAGTTT 4522

QY	1964	GCAGGCTCTGGTAAGAAGTGGAAAAAGGCACTGTAATAAGCCAGGCTTCACCTTAACAACA	2023
Db	4523	GCAGGCTCTGGTAAGAAGTGGAAAAAGGCACTGTAATAAGCCAGGCTTCACCTTAACAACA	4582
QY	2024	TATGCAAAATATTTCCATCCCTGAAATTACTTAGCCACAAAGCTATGGGAATGSCAGTGT	2083
Db	4583	TATGCAAAATATTTCCATCCCTGAAATTACTTAGCCACAAAGCTATGGGAATGSCAGTGT	4642
QY	2084	CACGGAATTAACAAGTGTAGTAGATAGAAAGAAGTGTGTGTGTATTGAATATATATCA	2143
Db	4643	CACGGAATTAACAAGTGTAGTAGATAGAAAGAAGTGTGTGTGTATTGAATATATATCA	4702
QY	2144	CACGAGATTTGTCTTCATTCGAGATGACAGTGTGTTACCTCTCCCTGTCCCTTGAACAC	2203
Db	4703	CACGAGATTTGTCTTCATTCGAGATGACAGTGTGTTACCTCTCCCTGTCTTGTGACAC	4762
QY	2204	GTCCTTTATTAATTTCCGTTCTCTCCCGGTTCCCAACGTTAAAAAAAAGTCACAGGCAAT	2263
Db	4763	GTCCTTTATTAATTTCCGTTCTCTCCCGGTTCCCAACGTTAAAAAAAAGTCACAGGCAAT	4822
QY	2264	ATTCTCCCTGAGGAGATPAAGGCTGSACTGTAGATGATPAACGAGATACCGTTTGTGTGT	2323
Db	4823	ATTCTCCCTGAGGAGATPAAGGCTGSACTGTAGATGATPAACGAGATACCGTTTGTGTGT	4882
QY	2324	TGTTGTGTCGTCGTTGTCTGTTGTTTGGACACGAGTCGTGCTCTGTCCGCCAGGCTGG	2383
Db	4883	TGTTGTGTCGTCGTTGTGTTGTTTGGACACGAGTCGTGCTCTGTCCGCCAGGCTGG	4942
QY	2384	AGTGCATATGGCGCGACGAAACGAGATGATGTTTTTAAAAACGAAGACACACTGSGTCTTCTT	2443
Db	4943	AGTGCATATGGCGCGACGAAACGAGATGATGTTTTTAAAAACGAAGACACACTGSGTCTTCTT	5002
QY	2444	CCATCAATATAGCAATPAATTTGGGAACTGACACCCAGACCTGTCCACTTCAGGCTC	2503
Db	5003	CCATCAATATAGCAATPAATTTGGGAACTGACACCCAGACCTGTCCACTTCAGGCTC	5062
QY	2504	CTATATGCTTCCTTTTCTCATCTCCTATTTGCCACTCTGGGATGCTGACACGATTTAAGAT	2563
Db	5063	CTATATGCTTCCTTTTCTCATCTCCTATTTGCCACTCTGGGATGCTGACACGATTTAAGAT	5122
QY	2564	TTGGCAGATATATGAGGCGAGGAGTGTGGAATTCCTCTCCCGCAAGTTTTCACACCC	2623
Db	5123	TTGGCAGATATATGAGGCGAGGAGTGTGGAATTCCTCTCCCGCAAGTTTTCACACCC	5182
QY	2624	CAGTTTGTCTGGGTGTGAGCGGAGTTATTTGTATCAACCTTGATCTGACCGGCA-GGA	2682
Db	5183	CAGTTTGTCTGGGTGTGAGCGGAGTTATTTGTATCAACCTTGATCTGACCGGCA-GGA	5242
QY	2683	TCTGTGTGTGTAAAGTGATGATCTCTGATGCTCTGTGTGACAAAAGAAGCTCGAATGCANAAGA	2742
Db	5243	TCTGTGTGTGTAAAGTGATGATCTCTGATGCTCTGTGTGACAAAAGAAGCTCGAATGCANAAGA	5302
QY	2743	CGCTGAGCTAAGAGGAGAGAGGCGCGGAGACCCAGAGGAAGAAGCACTCTCGGCGTTG	2802
Db	5303	CGCTGAGCTAAGAGGAGAGAGGCGCGGAGACCCAGAGGAAGAAGCACTCTCGGCGTTG	5362
QY	2803	GGGAAATTAAGAAGGAGGAGGCTTGAAGTGGGAGGGAAAGAGCCTGTGTAAGCGAC	2862
Db	5363	GGGAAATTAAGAAGGAGGAGGCTTGAAGTGGGAGGGAAAGAGCCTGTGTAAGCGAC	5422
QY	2863	TCAACAGAGGGAATAATATAAGGGAAGTGAAGAGAGGAAGAAGGAGACTGAAAGGGAAGGCGAG	2922
Db	5423	TCAACAGAGGGAATAATATAAGGGAAGTGAAGAGAGGAAGAAGGAGACTGAAAGGGAAGGCGAG	5482
QY	2923	TGGGAGAAAGGAGGAGCGAAAGAGGCGAAGAGAGGAAGAGAGGAGAGAGAGGAGGAGGA	2982
Db	5483	TGGGAGAAAGGAGGAGCGAAAGAGGCGAAGAGAGGAAGAGAGGAGAGAGAGGAGGAGGA	5542
QY	2983	GAGGGAAGGAAGGAATATGGGAGAGAGAGAGGCTCACAGATGTGACCTGTGACGATGGGCGCTTC	3042
Db	5543	GAGGGAAGGAAGGAATATGGGAGAGAGAGAGGCTCACAGATGTGACCTGTGACGATGGGCGCTTC	5602

	QY	3043 TCG 3045
Dd	5603 TCG 5605	
	RESULT 3	
	US-60-500-315-11863	
	: Sequence 11863, Application US/60500315	
	: GENERAL INFORMATION:	
	: APPLICANT: CARGILL, Michele	
	: TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES	
	: : TITLE OF INVENTION: ENCODING HUMAN G-PROTEIN COUPLED RECEPTOR PROTEINS, METHODS	
	: FILE REFERENCE: CL001484	
	: CURRENT APPLICATION NUMBER: US/60/500,315	
	: CURRENT FILING DATE: 2003-09-05	
	: NUMBER OF SEQ ID NOS: 69978	
	: SOFTWARE: FastSeq for Windows Version 4.0	
	: SEQ ID NO 11863	
	: LENGTH: 14011	
	: TYPE: DNA	
	: ORGANISM: Homo sapiens	
	US-60-500-315-11863	
Query Match	89.7%; Score 2731; DB 107; Length 14011;	
Best Local Similarity	97.4%; Pred. No. 0;	
Matches 2984; Conservative	5; Mismatches 45; Indels 29; Gaps 20;	
QY	1 ATCATCAATAATCCGTTAATAAGCTTGTCTTCCTTAGGTTACTTAAGGGCCTTGA	60
Dd	723 ATATCAATAAATCCGTAAATAAGCTTGCTTCCTTAGGTTAACCTTAGAGGCCTTGA	782
QY	61 AGAATAAGAGCTCATCTCTTTA--CAGAAGCTTGGTTGACATTACTTAGAATA	118
Dd	783 AQAATAAGAGCTCATCTCTTTANCGAGAGCTTGGTTGACGAATTAATAAGAAATA	842
QY	119 TTGGTAATCTGTATCTTTAAGATTAAACAATAGAAATGGCTAAGTGAATAATG	178
Dd	843 TTGGTAATCTGTATCTTTAAGATTAAACAATAGAAATGGCTAAGTGAATAATG	901
QY	179 AAAGCAATTCATCTTCGATATATCATTTATATATATACAGATTATTAAGTTTT-AA	237
Dd	902 AAAGCAATTCATCTTCGATATATATATATATATATATATACAGATTATTAAGTTTTAAA	961
QY	238 AAGTTAAACATAAANAATCTATATGTCATGSCAGATAGSYAACTPRTCRGTGCTGC	297
Dd	962 AAGTTAAACATAAANAATCTATTA-GTCACTTGCAAGCTATGGAACATPATGTACGTGCTGC	1020
QY	298 GAATACCTTCGACATCTGTCTGCCCTCCTAGATTCATAAAGTGGCCTTGAAACGTT	357
Dd	1021 ATA--CTTCACATCTGTCTGCCCTCCTAGATTCATAAAGTGGCCTTGAAACG-TT	1076
QY	358 TTAATTTGTAGAATAATAATGTTTGATATATATATATATTAATAAGAAAAAACC	417
Dd	1077 TTAATTTGTAGAATAATAATGTTTGATATATATATATATTAATAAGAAAAAACC	1136
QY	418 GAATTAATCTTGCATTTTGAAAAAACCCTTGATAATTTACATATAGCATATTGAAGCAAG	477
Dd	1137 GAATTAATCTTGCATTTTGAAAAAACCCTTGATAATTTACATATAGCATATTGAAGC-A	1195
QY	478 AATAACAATAAGCATACCTCAGGAATATTAATCCAGATTTCACAGCATTTTAACTTTCT	537
Dd	1196 AATAACAATAAGCATACCTCAGGAATATTAATTTCCAGATTTCACAGCATTTTAACTTTCT	1255
QY	538 TGATGAGAAAAATAAATTTTGCAATTATTAACATAATT--GATCCAACAGATGAAGA	596
Dd	1256 TGATGAGAAAAATAAATTTTGCAATTATTAACATAATTGGATCCAAACAGATGAAGA	1315
QY	597 GAATTCATACTAATATTTATGATTTATTTGTGATTACATATTAATCATGAGTGTGTT	656
Dd	1316 GAATTCATACTAATATTTATGATTTATTTGTGATTACATATTTACATGAGTGTGTT	1375
QY	657 GACACAATCTTAATATATGTTCTTGATATGACATAATTTGCTTTAAATTTAAAGTTTC	716

Db	1376	GACGCAATTCCTTAATTATGCTTGTAATGCAATATTTGCTTAAATTTAAGTTTC	1435
Qy	717	CTTAATTTACTTTGTTTAATAGTCAACATAATTTCAAGTTAATTTAGATAATTC	776
Db	1436	CTTAATTTTACTTTGTTAATAGTCAACATAATTTCAAGTTAATTTAGATAATTC	1495
Qy	777	AGCCTTTAAATATTTTCCCATTAATATTTTGGAACCTCAACCTAATTTTAAGTGA	836
Db	1496	AG-CTTTAAATATTTTCCCATTAATATTTTG-GACCTCAACCTAATTTTAAGTGA	1553
Qy	837	ATATAGTCTGTAATTTGTGAAGAGACTTAGAAGTGAATAGATACCTTCACAATCTT	896
Db	1554	ATATAGTCTGTAATTTGTGAAGAGACTTAGAAGTGAATAGATACCTTCACAATCTT	1613
Qy	897	-AAAAAGACTTCTTCAGAGTCTGTAAACAGCATTAACATGTAATCTATATCTTCTTTC	955
Db	1614	AAAAAGACTTCTTCAGAGTCTGTAAACAGCATTAACATGTAATCTATATCTTCTTTC	1673
Qy	956	ATGCC---ATGATCATCAACATGATGGCTCATGCTGGGCATGCTG-AATGATAGT	1010
Db	1674	ATGCGATGAATCATCAACAAATGCGAGCTATGTGGTGCATGCTGAATGATGAT	1733
Qy	1011	GGGACTGTGCC--AGCTGAACATAAAAAAACAACAAACAAACCTTATCCAAACA	1066
Db	1734	GGGAAGTGTGCCAGCACTGAACATAAAAAAACAACAAACCTTATCCAAACA	1793
Qy	1067	CAGTGCCTGTAATGTGAATGCAATGGCCCACTGGAATCTTTTGAAGCTTGGTGAATG	1126
Db	1794	CAGTGCCTGTAATGTGAATGCAATGGCCCACTGGAATCTTTTGAAGCTTGGTGAATG	1853
Qy	1127	CTCTTTTGTGGGCTGGAGAAATCAGAGCTATGAATTCAGAGCTCAGATTTGAACAC	1186
Db	1854	CTCTTTTGTGGGCTGGAGAAATCAGAGCTATGAATTCAGAGCTCAGATTTGAACAC	1913
Qy	1187	AATATTAAGATTAATTTGCAATCTGTATGAATCTGTCAATGTTTACAGTGTCACTGTT	1246
Db	1914	AATATTAAGATTAATTTGCAATCTGTATGAATCTGTCAATGTTTACAGTGTCACTGTT	1973
Qy	1247	TTGAGATTGCATTCCTTCACTCAGAGATCAATCAGAGTGAATGAATGAATGGTGTG	1306
Db	1974	TTGAGATTGCATTCCTTCACTCAGAGATCAATCAGAGTGAATGAATGAATGGTGTG	2033
Qy	1307	TGTAATGTTTACTGTATGTTGCTTAGAGT-CCATTCCTTACCAATGCTCAAAATGTATTA	1365
Db	2034	TGTAATGTTTACTGTATGTTGCTTAGAGT-CCATTCCTTACCAATGCTCAAAATGTATTA	2093
Qy	1366	AATTTG-TTTACTGTTAAGGAAACAGCTTAGAACAAACCTGTGAATGTTCTTA-TT	1423
Db	2094	AATTTGTTTCTTTCTTTTAAAGGAAACAGCTTAGAACAAACCTGTGAATGTTCTTA-TT	2153
Qy	1424	TCAGTGAATTTAACATTTCCAAATGTTAATCATTTTGAAAAATGCAATATCTATCGTTCT	1483
Db	2154	TCAGTGAATTTAACATTTCCAAATGTTAATCATTTTGAAAAATGCAATATCTATCGTTCT	2213
Qy	1484	CCAACAAAGGTAATTTATGTCAGTCCCAAGTCAAGTTATGACAGCAACAAACCAAC	1543
Db	2214	CCAACAAAGGTAATTTATGTCAGTCCCAAGTCAAGTTATGACAGCAACAAACCAAC	2273
Qy	1544	ACAGGTGAAGTGTAGCTAGCTTATTAATAATGGCAATCCCAATTGGAACCTGTGAT	1603
Db	2274	ACAGGTGAAGTGTAGCTAGCTTATTAATAATGGCAATCCCAATTGGAACCTGTGAT	2333
Qy	1604	GACAGATATCTTCAGGCTTTCCAGAGAGACTAAACATATATAGGCTCGATATATAAGT	1663
Db	2334	GACAGATATCTTCAGGCTTTCCAGAGAGACTAAACATATATAGGCTCGATATATAAGT	2393
Qy	1664	TCAGAGCAAAAGAGGCACTAAATTAATTTTAAAGAAATAGGAAGAGACAAAATCC	1723
Db	2394	TCAGAGCAAAAGAGGCACTAAATTAATTTTAAAGAAATAGGAAGAGACAAAATCC	2453
Qy	1724	AATACTACTTGTCTTTAATATAGTGTCTCTCTTTCTAAAGTGTGTGATTTCTCTCA	1783

Db	2451	AATACTACCTTGGCTTTTAAATACAGCTCTCCCTTTCTTAAAGTGTGTATTTCTCTCA	2513
QY	1784	ATACTTGGCTTCATTTCTGGCAATTAAGGGTTTCCAGATGGCACTCTTAAACATTTGGCCGAA	1843
Db	2514	ATACTTGGCTTCATTTCT-GGATTAAGGGTTTCCAGATGGCACTCTTAAACATTTGGCCGAA	2572
QY	1844	GGTGGCGCACTAAATACCTCATTTGCTTAAAGATCTGTCCAGATGTGTGAACCCAGTTTCTGA	1903
Db	2573	GGTGGCG-ACCTTAATACCTCATTTGCTTAAAGATCTGTCCAGATGTGTGAACCCAGTTTCTGA	2631
QY	1904	GATTAAAGAGGCTAGCCGGCTAGCGAGATTCACCAAGTTTCCCCAGAGGTTT	1963
Db	2632	GATTAAAGAGGCTAGCCGGCTAGCGAGATTCACCAAGTTTCCCCAGAGGTTT	2691
QY	1964	GCAGGCTCTGGTAGAAGTGCMAAAGCCATGTGAATGCGAGGCTTCACCTTAAACACA	2023
Db	2692	GCAGGCTCTGGTAGAAGTGCMAAAGCCATGTGAATGCGAGGCTTCACCTTAAACACA	2751
QY	2024	TATGCAAAATTTTCCATCCCTGATTTACTAGCCACMAAGCTATGGAAATGGCAGTGT	2083
Db	2752	TATGCAAAATTTTCCATCCCTGATTTACTAGCCACMAAGCTATGGAAATGGCAGTGT	2811
QY	2084	CACCTGAATTAACAAGTGTATGTATGTATGTGAAGAAAGTGTGTGTGTATTAAGATATATATCA	2143
Db	2812	CACCTGAATTAACAAGTGTATGTATGTATGTGAAGAAAGTGTGTGTGTATTAAGATATATATCA	2871
QY	2144	CACAGAGTTTGTCTTCATTCATTCAGATGTAGATGTGTAACTCTCTGTCTCTTTGACAC	2203
Db	2872	CACAGAGTTTGTCTTCATTCATTCAGATGTAGATGTGTAACTCTCTGTCTCTTTGACAC	2931
QY	2204	GTCCTTAAATTTGCTTCTCTCCGGTCCCAAGTTAAAAAAAAGTCACAGGCAT	2263
Db	2932	GTCCTTAAATTTTGGTCTCTCCGGTCCCAAGTTAAAAAAAAGTCACAGGCAT	2991
QY	2264	ATTCTCCCTGAGGAGTAAGGCTGGACTGTATATGTATTAACGAGATACGTTTGTGTGT	2333
Db	2992	ATTCTCCCTGAGGAGTAAGGCTGGACTGTATATGTATTAACGAGATACGTTTGTGTGT	3051
QY	2334	TGTTGTGTCGTCGTTTGTGTTTGTGTAAGCAGAGTCTGCTGTGTGCGCCAGGCTGG	2383
Db	3052	TGTTGTGTCGTCGTTTGTGTTTGTGTAAGCAGAGTCTGCTGTGTGCGCCAGGCTGG	3111
QY	2384	AGTCACATGGGCGAGAAACGAGGTACTTTTAAACAGAAAGACACATGGACTTCTT	2443
Db	3112	AGTCACATGGGCGAGAAACGAGGTACTTTTAAACAGAAAGACACATGGACTTCTT	3171
QY	2444	CCATCAATTAACAATAATTGGGAGATCAGCCAGAGCTGTCACTTCCCATTTGAGGCTC	2503
Db	3172	CCATCAATTAACAATAATTGGGAGATCAGCCAGAGCTGTCACTTCCCATTTGAGGCTC	3231
QY	2504	CCATAGCTTCTTTTCTCATCTCTATTTGCCACTCTGGAGTGTGACACAGATTTAAAGAT	2563
Db	3232	CCATAGCTTCTTTTCTCATCTCTATTTGCCACTCTGGAGTGTGACACAGATTTAAAGAT	3291
QY	2564	TTGCAAGATATATGAGGCAAGAGTGTGGAATTTCCCTCCCAAGTTTTCACACCC	2623
Db	3292	TTGCAAGATATATGAGGCAAGAGTGTGGAATTTCCCTCCCAAGTTTTCACACCC	3351
QY	2624	CAGTTTGTCTGGGTGAGGCGGAGTTTATTTGTTACAACCTTGTGTGACCGGCA-GGA	2682
Db	3352	CAGTTTGTCTGGGTGAGGCGGAGTTTATTTGTTACAACCTTGTGTGACCGGAGGGA	3411
QY	2683	TCTGTGTGTATAGTAGTGTCTGAGTCTGTGTGACAAAAGAGACTGCAATTCGAAGA	2742
Db	3412	TCTGTGTGTATAGTAGTGTCTGAGTCTGTGTGACAAAAGAGACTGCAATTCGAAGA	3471
QY	2743	CGCTGAGCTAGAGGAGAGGAGCGGAGCCACAGAGAAAAGGCACTCTCGGGGTG	2802
Db	3472	CGCTGAGCTAGAGGAGAGGAGCGGAGCCACAGAGAAAAGGCACTCTCGGGGTTG	3531
QY	2803	GGGAAGATTAAGAGGGGAGGGGTTAAGGTGGGAAGGAAGGAGCTGTGTTTGAAGCGAC	2862
Db	3532	GGGAAGATTAAGAGGGGAGGGGTTAAGGTGGGAAGGAAGGAGCTGTGTTTGAAGCGAC	3591

Db	4318	ACAGGTAAAGTGTTAAGCTTAAGCTTTATTAATATGCAATTCGCCAGTTAGAACTTGTAAT	4377
QY	1604	GAACAGTACTTCAGGCTTTGCAAGAAAGCTAAAACATATATATAGGCTGATATATAAAGT	1663
Db	4378	GACAGTACTTCAGGCTTTGCAAGAAAGCTAAAACATATATATAGGCTGATATATAGGT	4437
QY	1664	TCGAGAGAAAAGGGGACCTPAAATTAATTTTAAAGAAAATAGAAAGGAGACAAAATCTC	1723
Db	4438	TCGAGAGAAAAGGGGACCTPAAATTAATTTTAAAGAAAATAGAAAGGAGACAAAATCTC	4497
QY	1724	AATATCACTGTGCTTTTAAATPACTGTCTTCCCTTTCTPAAAGTTGTGTATTTCTCA	1783
Db	4498	AATATCACTGTGCTTTTAAATPACTGTCTTCCCTTTCTPAAAGTTGTGTATTTCTCA	4557
QY	1784	ATATCTTGCTTCATTTCTGCGCATTAAGGGTTTCCAAATGCGACTCTMAAACATTTGCCGAA	1843
Db	4558	ATATCTTGCTTCATTTCTGCGCATTAAGGGTTTCCAAATGCGACTCTMAAACATTTGCCGAA	4616
QY	1844	GGTGGCGAACATAAACTCATTCGTTAGAACTGCCAGGTGCTGAAACCCAGTTTCTGA	1903
Db	4617	GGTGGCGGACATAAACTCATTCGTTAGAACTGCCAGGTGCTGAAACCCAGTTTCTGA	4675
QY	1904	GATTAAAGAGAGCTAGCCGCGCTAGCCGAAACCGGAAITTCACCAAGTTTCCCACAGGTTT	1963
Db	4676	GATTAAAGAGAGCTAGCCGCGCTAGCCGAAACCGGAAITTCACCAAGTTTCCCACAGGTTT	4735
QY	1964	GCAAGGCTCTGGTAAGAGAGTGCAAAAGGCAATGTAAATGCCAGGCTCAGTTAAGAACCA	2023
Db	4736	GCAAGGCTCTGGTAAGAGAGTGCAAAAGGCAATGTAAATGCCAGGCTCAGTTAAGAACCA	4795
QY	2024	TATGCAAAATATTTTCCATCCCTGCAATTTACTATGCAACAAAGCTATGCGAAGTGGCAGGT	2083
Db	4796	TATGCAAAATATTTTCCATCCCTGCAATTTACTATGCAACAAAGCTATGCGAAGTGGCAGGT	4855
QY	2084	CACCTGAATTAACAAGTGTAGTATGTATGAGAAAAGTGTGTGTGTATTAAGATATATATATCA	2143
Db	4856	CACCTGAATTAACAAGTGTAGTATGTATGAGAAAAGTGTGTGTGTATTAAGATATATATCA	4915
QY	2144	CACAGAGTTTGTCTTCATTTGCGAGTACGAGTGTATTCCTCTCTTGTCCCTTGAACAC	2203
Db	4916	CACAGAGTTTGTCTTCATTTGCGAGTACGAGTGTATTCCTCTCTTGTCCCTTGAACAC	4975
QY	2204	GTCCTTTATATTTTCGTCTCTCCCGGTTCCCAACGTTAAAAAAAAGTCAACAGGCAT	2263
Db	4976	GTCCTTTATATTTTCGTCTCTCCCGGTTCCCAACGTTAAAAAAAAGTCAACAGGCAT	5035
QY	2264	ATTCCCTCGAGGAGTAAAGGTGACCTGTATAGTAAAGAGAGTACCGTTTGTGT	2323
Db	5036	ATTCCCTCGAGGAGTAAAGGTGACCTGTATAGTAAAGAGAGTACCGTTTGTGT	5095
QY	2324	TGTTGTGCTGCTGTGTGCTTTGTTTGAAGACGAGTCTGCTGTGCTGCTGCCAGGCTGG	2383
Db	5096	TGTTGTGCTGCTGTGTGCTTTGTTTGAAGACGAGTCTGCTGTGCTGCTGCCAGGCTGG	5155
QY	2384	AGTGAATAGGGGCGAGAACGAGAGTATTTTAAAAAGAAAGACACTCGGCTTCTT	2443
Db	5156	AGTGAATAGGGGCGAGAACGAGAGTATTTTAAAAAGAAAGACACTCGGCTTCTT	5215
QY	2444	CCATCAATTAAGCAATATTTGGAGACTGACCCAGGACTGTTCACTTCCATTACAGGCTC	2503
Db	5216	CCATCAATTAAGCAATATTTGGAGACTGACCCAGGACTGTTCACTTCCATTACAGGCTC	5275
QY	2504	CCTATAGCTTCTTTTCTCATCTCCCTATTTGCCACTGTGGAGAGCTGACACAGATTAAGAT	2566
Db	5276	CCTATAGCTTCTTTTCTCATCTCCCTATTTGCCACTGTGGAGAGCTGACACAGATTAAGAT	5336
QY	2564	TTGGCAGATTAATATAGGCAAGAGATAGTGAATTCCTCCGCCAGGTTTTCACACC	2623
Db	5336	TTGGCAGATTAATATAGGCAAGAGATAGTGAATTCCTCCGCCAGGTTTTCACACC	5395
QY	2624	CAGTTTGTGCTGGGTTGAGGCGGAGTTTATTTGTTACAACTTGCTGACCCGGCAAGCA	2682

Db	5396	CAGTTTGTGCGGTGGAGGCGGAGTTTATTGTGTACAACTTGCTGTGACCCGCAAGGA	5455
Qy	2683	TCCTGTGTGTGTACGTACGAGTTCTTGAAGTCTGTGTGACAAAAGAGACTCGAATGCAAGA	2742
Db	5456	TCCTGTGTGTGTGTAAGTAGTCTTGAAGTCTGTGTGTGACAAAAGAGACTCGAATGCAAGA	5515
Qy	2743	CGCTGAGCTGAGGAGAGAGAGGCGGGGACCCAGAGAAAAGAGCACTCTCGGGGTTG	2802
Db	5516	CGCTGAGCTGAGGAGAGAGAGGCGGGGACCCAGAGAAAAGAGCACTCTCGGGGTTG	5575
Qy	2803	GCGAAGTATTAGAGAGGGAAGGTTTAAAGTGGAGAGGAAGAGCTTGCTTTCGAGGAC	2862
Db	5576	GCGAAGTATTAGAGAGGGAAGGTTTAAAGTGGAGAGGAAGAGCTTGCTTTCGAGGAC	5635
Qy	2863	TCACAGAGGATTAATTAAGGAAGTATAGAGAGGAAGAGAGACTGAAGGGAAGGACG	2922
Db	5636	TCACAGAGGATTAATTAAGGAAGTATAGAGAGGAAGAGAGACTGAAGGGAAGGACG	5695
Qy	2923	TGGGAGAGAGGGGAGCGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGGGGGAGA	2982
Db	5696	TGGGAGAGAGGGGAGCGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGGGGGAGA	5755
Qy	2983	GAGGGAAGGAAGGAATATAGGAGAGAGAGGCTCAGAGTGAACGTTGAGAGTGGGCTTC	3042
Db	5756	GAGGGAAGGAAGGAATATAGGAGAGAGAGGCTCAGAGTGAACGTTGAGAGTGGGCTTC	5815
Qy	3043	TCG 3045	
Db	5816	TCG 5818	
RESULT 5			
US-60-205-423-94			
; Sequence 94, Application: US/60205423			
; GENERAL INFORMATION:			
; APPLICANT: Beasley, Ellen			
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED			
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR			
; FILE REFERENCE: CL000563			
; CURRENT APPLICATION NUMBER: US/60/205,423			
; CURRENT FILING DATE: 2000-05-19			
; NUMBER OF SEQ ID NOS: 494			
; SOFTWARE: PasteSeq for Windows Version 4.0			
; SEQ ID NO 94			
; LENGTH: 2112			
; TYPE: DNA			
; ORGANISM: HUMAN			
US-60-205-423-94			
Query Match			
Best Local Similarity 99.64; Pred. No. 5e-230; Mismatches 1; Indels 5; Gaps 5			
Matches 1437; Conservative 0			
Qy	1606	CAGATACTTCAGGCTTTCGAAGAAGCT-AAACATATATAGGCTGTGATATATAGGTT	1666
Db	2	CAGATACTTCAGGCTTTCGAAGAAGCTAAACATATATAGGCTGTGATATATAGGTT	61
Qy	1665	CAGAGCAAAAAGGGCACTAAATTAATTTTAAAGAAATA-GAAGGAGACAAAATC	1723
Db	62	CAGAGCAAAAAGGGCACTAAATTAATTTTAAAGAAATAAGGAGAGACAAAATC	121
Qy	1724	AATATCACTTGTCTTTTAAATAGCTGTCTCTCTTTCTAAAGTGTGTATTTCTCA	1783
Db	122	AATATCACTTGTCTTTTAAATAGCTGTCTCTCTTTCTAAAGTGTGTATTTCTCA	181
Qy	1784	ATACTTGTTCAATTTCGTGGCATAGGGTTTCAGATGGCACTTAAACATTTGGCAGAA	1844
Db	182	ATACTTGTTCAATTTC-GCATTAAGGGTTTCCAGATGGCACTTAAACATTTGGCAGAA	240
Qy	1844	GATGGCGCAACATAAAACCTCATTTGTAAGACTGTCCAGAGTGTGAACCCAGTTTCTGA	1903
Db	241	GATGGCGC-ACATTAACCTCATTTGTTAAGACTGTCCAGAGTGTGAACCCAGTTTCTGA	299


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Db      181  CCATCAATTACCAATTAATGGAGACTGACCCAGAGCTGTCACCTCCCATCGAGCTC 240
Qy      2504  CCTAGCTCTCTTTTCTCATCTCCATTTGCACTCTGGAGTGCAGACAGATTAATAAT 2563
Db      241  CCTAGCTCTCTTTTCTCATCTCCATTTGCACTCTGGAGTGCAGACAGATTAATAAT 300
Qy      2564  TTGGCAGATAATATGAGGCAAGAGTAGTGAATTCCTCCCTCCCAAGTTTTCACACC 2623
Db      301  TTGGCAGATAATATGAGCAGAGAGTAGTGAATTCCTCCCTCCCAAGTTTTCACACC 360
Qy      2624  CAGTTTCTCTGGTTGGAGGCGGAGTTTATTTTTCACACTTGTCTGACCGCA  GGA 2682
Db      361  CAGTTTCTCTGGTTGGAGGCGGAGTTTATTTTTCACACTTGTCTGACCGCA  GGA 420
Qy      2683  TCTGTGTGTGTAGTAGTCTGAGTCTCTGTTCACAAAAGAGACTGCAATGCAAGA 2742
Db      421  CTTGTGTGTGTAGTAGTCTGAGTCTCTGTTCACAAAAGAGACTGCAATGCAAGA 480
Qy      2743  CGCTGAGCTTAGAGGAGAGAGAGGCGGAGCCAGAGAGAAAGAGCACTCTCGGGGTTG 2802
Db      481  CGCTGAGCTTAGAGGAGAGAGAGGCGGAGCCAGAGAGAAAGAGCACTCTCGGGGTTG 540
Qy      2803  GGGAGAGTTTAGAGGAGGAGGTTAGAGTGGAGAGGAAAGAGCCTGCTTCGAGAGAC 2862
Db      541  GGGAGAGTTTAGAGGAGGAGGTTAGAGTGGAGAGGAAAGAGCCTGCTTCGAGAGAC 599
Qy      2863  TCACAGAGGATTAATTAAGGAGAGTAGAGAGAGAGAGAGACTGAAGAGGAAAGGAGG 2922
Db      600  TCACAGAGGATTAATTAAGGAGAGTAGAGAGAGAGAGAGAGACTGAAGAGGAAAGGAGG 659
Qy      2923  TGGGAGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2982
Db      660  TGGGAGAGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
Qy      2983  GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3042
Db      720  GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 779
Qy      3043  TCG 3045
Db      780  TCG 782

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RESULT 9
US-10-049-407-3
; Sequence 3, Application US/10049407
; GENERAL INFORMATION:
; APPLICANT: Denton, R. Rex
; APPLICANT: Kilem, Stefanie
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: DRUG TARGET ISOGENES: POLYMORPHISMS IN THE
; TITLE OF INVENTION: 5-HYDROXYTRYPTAMINE RECEPTOR 1A GENE
; FILE REFERENCE: MMH-000605 HTR1A
; CURRENT APPLICATION NUMBER: US/10/049,407
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: PCT/US00/40519
; PRIOR FILING DATE: 2000-08-06
; PRIOR APPLICATION NUMBER: 60/147,711
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-049-407-3

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Query Match      24.6%; Score 747.8; DB 43; Length 2722;
Best Local Similarity 98.9%; Pred. No. 9.7e-120;
Matches 774; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Qy      2264  ATTCTCCCTGAGGAGATTAAGGCTGAGCTGTATGATATACGAGAGTACCGTTTGTGT 2323
Db      1  ATTCTCCCTGAGGAGATTAAGGCTGAGCTGTATGATATACGAGAGTACCGTTTGTGT 60
Qy      2324  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2383
Db      61  TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy      2384  AGTGCATGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2443
Db      121  AGTGCATGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy      2444  CCATCAATTACCAATTAATGGAGACTGACCCAGAGCTGTTACCTTCCATTCAGGCTC 2503
Db      181  CCATCAATTACCAATTAATGGAGACTGACCCAGAGCTGTTACCTTCCATTCAGGCTC 240
Qy      2504  CCTAGCTCTCTTTTCTCATCTCCATTTGCACTCTGGAGTGTGACAGATTTAGAAAT 2563
Db      241  CCTAGCTCTCTTTTCTCATCTCCATTTGCACTCTGGAGTGTGACAGATTTAGAAAT 300
Qy      2564  TTGGCAGATAATATGAGGCAAGAGTAGTGAATTCCTCCCTCCCAAGTTTTCACACC 2623
Db      301  TTGGCAGATAATATGAGCAGAGAGTAGTGAATTCCTCCCTCCCAAGTTTTCACACC 360
Qy      2624  CAGTTTCTCTGGTTGGAGGCGGAGTTTATTTTTCACACTTGTCTGACCGCA  GGA 2682
Db      361  CAGTTTCTCTGGTTGGAGGCGGAGTTTATTTTTCACACTTGTCTGACCGCA  GGA 420
Qy      2683  TCTGTGTGTGTAGTAGTCTGAGTCTCTGTTCACAAAAGAGACTGCAATGCAAGA 2742
Db      421  CTTGTGTGTGTAGTAGTCTGAGTCTCTGTTCACAAAAGAGACTGCAATGCAAGA 480
Qy      2743  CGCTGAGCTTAGAGGAGAGAGGCGGAGCCAGAGAGAAAGAGCACTCTCGGGGTTG 2802
Db      481  CGCTGAGCTTAGAGGAGAGAGGCGGAGCCAGAGAGAAAGAGCACTCTCGGGGTTG 540
Qy      2803  GGGAGATTAATTAAGGAGGAGGTTAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2862
Db      541  GGGAGATTAATTAAGGAGGAGGTTAGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
Qy      2863  TCACAGAGGATTAATTAAGGAGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2922
Db      600  TCACAGAGGATTAATTAAGGAGAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
Qy      2923  TGGGAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2982
Db      660  TGGGAGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
Qy      2983  GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3042
Db      720  GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 779
Qy      3043  TCG 3045
Db      780  TCG 782

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RESULT 10
US-09-541-946-2477
; Sequence 2477, Application US/09541946
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Altschuler, David M.
; APPLICANT: Ireland, James S.
; APPLICANT: Sklar, Pamela
; APPLICANT: Patil, Nila
; APPLICANT: Lipschutz, Robert J.
; APPLICANT: Daley, George Q.
; TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES
; FILE REFERENCE: 2825.1017-003
; CURRENT APPLICATION NUMBER: US/09/541,946

```

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/ CURRENT FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: US 60/127,248
/ PRIOR FILING DATE: 1999-03-31
/ NUMBER OF SEQ ID NOS: 2889
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2477
/ LENGTH: 839
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-541-946-2478

Query Match      24.4%; Score 742.4; DB 23; Length 839;
Best Local Similarity 98.7%; Pred. No. 6.3e-119;
Matches 768; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

QY 2269 CCTGAGGAGTAAGGCTGAGCTGATGATGATACGAGAGTACCGTTTGTGTGTG 2328
DB 1 CCTGAGGAGTAAGGCTGAGCTGATGATGATGATGATGATGATGATGATGATG 60
QY 2329 TCGTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2388
DB 61 TCGTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
QY 2389 AATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2448
DB 121 AATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 2449 AATTAGCAATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2508
DB 181 AATTAGCAATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 2509 GCTTCCTTTCTCATCTCCATATGCGACCTGCGAGTCTGACAGATTAAGAATTG 2568
DB 241 GCTTCCTTTCTCATCTCCATATGCGACCTGCGAGTCTGACAGATTAAGAATTG 300
QY 2569 AGATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2628
DB 301 AGATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 2629 TTGCTGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2687
DB 361 TTGCTGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 2688 TGTGTGAAGTGAAGTCTGAGTCTCTGTTGACAAAAGAGAGAGAGAGAG 2747
DB 421 TGTGTGAAGTGAAGTCTGAGTCTCTGTTGACAAAAGAGAGAGAGAGAG 480
QY 2748 AGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2807
DB 481 AGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 2808 GTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2867
DB 541 GTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
QY 2868 GAGGGAATTAATAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2927
DB 600 GAGGGAATTAATAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
QY 2928 AGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2987
DB 660 AGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
QY 2988 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3045
DB 720 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777

RESULT 11
US-09-541-946-2478
/ Sequence 2478, Application US/09541946
/ GENERAL INFORMATION:
/ APPLICANT: Lander, Eric S.
```

```
/ APPLICANT: Cargill, Michele
/ APPLICANT: Altschuler, David M.
/ APPLICANT: Ireland, James S.
/ APPLICANT: Sklar, Pamela
/ APPLICANT: Patel, Nila
/ APPLICANT: Lipschutz, Robert J.
/ APPLICANT: Daley, George Q.
/ TITLE OF INVENTION: CHARACTERIZATION OF SINGLE NUCLEOTIDE
/ TITLE OF INVENTION: POLYMORPHISMS IN CODING REGIONS OF HUMAN GENES
/ FILE REFERENCE: 2825, 1017-003
/ CURRENT APPLICATION NUMBER: US/09/541,946
/ CURRENT FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: US 60/127,248
/ PRIOR FILING DATE: 1999-03-31
/ NUMBER OF SEQ ID NOS: 2889
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2478
/ LENGTH: 839
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-541-946-2478

Query Match      24.4%; Score 742.4; DB 23; Length 839;
Best Local Similarity 98.7%; Pred. No. 6.3e-119;
Matches 768; Conservative 1; Mismatches 7; Indels 2; Gaps 2;

QY 2269 CCTGAGGAGTAAGGCTGAGCTGATGATGATACGAGAGTACCGTTTGTGTGTG 2328
DB 1 CCTGAGGAGTAAGGCTGAGCTGATGATGATGATGATGATGATGATGATGATG 60
QY 2329 TCGTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2388
DB 61 TCGTCGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 120
QY 2389 AATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2448
DB 121 AATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 2449 AATTAGCAATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2508
DB 181 AATTAGCAATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 2509 GCTTCCTTTCTCATCTCCATATGCGACCTGCGAGTCTGACAGATTAAGAATTG 2568
DB 241 GCTTCCTTTCTCATCTCCATATGCGACCTGCGAGTCTGACAGATTAAGAATTG 300
QY 2569 AGATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2628
DB 301 AGATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 2629 TTGCTGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2687
DB 361 TTGCTGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 2688 TGTGTGAAGTGAAGTCTGAGTCTCTGTTGACAAAAGAGAGAGAGAGAG 2747
DB 421 TGTGTGAAGTGAAGTCTGAGTCTCTGTTGACAAAAGAGAGAGAGAGAG 480
QY 2748 AGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2807
DB 481 AGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 2808 GTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2867
DB 541 GTATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
QY 2868 GAGGGAATTAATAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2927
DB 600 GAGGGAATTAATAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
QY 2928 AGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2987
DB 660 AGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
```


QY 898 AAGACTTCTTCAGAGTCTGTAACAGCATTCACATGATCTATCTCTTTCTTGCAAT 957
DB 261 AAGACTTCTTCAGAGTCTGTAACAGCATTCACATGATCTATCTCTTTCTTGCA 202
QY 958 GCC---ATGATCATCAACATGAGTCTGATGCTGATGCTGCG--AATGATGAGTGG 1012
DB 201 TGCCATGATATCATCAAAATGCGAGCTCATTTGGTGGCATGCTGTAATGATGAGTGG 142
QY 1013 GACTGTGCC---AGCTGACTATATAAAAAAACAACAAACCTTATCCAAACACA 1068
DB 141 GAACGTGCCAGCATGTAACATATAAAAAAACAACAAACCTTATCCAAACACA 82
QY 1069 CTGTCCGTATGTAATGATGAGTCTGCGCCCACTGATCTCTTTGATGCTTGATGCT 1128
DB 81 CTGTCCGTATGTAATGATGAGTCTGCGCCCACTGATCTCTTTGATGCTTGATGCT 22
QY 1129 CTTTGTGTTGGGCTTGAGAA 1149
DB 21 CTTTGTGTTGGGCTTGAGAA 1

RESULT 14
US-09-634-306B-196187/c
; Sequence 196187, Application US/09634306B
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/09/634, 306B
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196187
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-09-634-306B-196187

Query Match 14.1%; Score 428.2; DB 26; Length 559;
Best Local Similarity 92.2%; Pred. No. 2.7e-64;
Matches 517; Conservative 2; Mismatches 30; Indels 12; Gaps 6;
QY 599 ATTCTAACAATATTATGATTTATTTGATGATTTACATATTACATGTTGTTGA 658
DB 559 ATTCTAACAATATTATGATTTATTTGATGATTTACATATTACATGTTGTTGA 500
QY 659 CACAAATTTTAATATGTTCTTGATATGCAATATTTGCTTTAAATTTTAACTTCT 718
DB 499 CACAAATTTTAATATGTTCTTGATATGCAATATTTGCTTTAAATTTTAACTTCT 440
QY 719 TTAATTTACTTTGTTATAGTCTCACTATATTTCAAGTTTAAATTTAGATATTCAG 778
DB 439 TTAATTTACTTTGTTATAGTCTCACTATATTTCAAGTTTAAATTTAGATATTCAG 380
QY 779 CCTTTTAAATTTTCCCATATATTTTGTGACCTCTAATCTATATTTAACTGTAAT 838
DB 379 -CTTTTAAATTTTCCCATATATTTTGTG-GACCTCTAATCTATATTTAACTGTAAT 322

QY 839 ATATGTTCTGATTTTGTGAAGAGACTTTAGAAATAGATACCTTACAAATCTT-A 897
DB 321 AAGACTTCTTCAGAGTCTGTAACAGCATTCACATGATCTATCTCTTTCTTGCA 262
QY 898 AAGACTTCTTCAGAGTCTGTAACAGCATTCACATGATCTATCTCTTTCTTGCA 957
DB 261 AAGACTTCTTCAGAGTCTGTAACAGCATTCACATGATCTATCTCTTTCTTGCA 202
QY 958 GCC---ATGATCATCAACATGAGTCTGATGCTGATGCTGCG--AATGATGAGTGG 1012
DB 201 TGCCATGATATCATCAAAATGCGAGCTCATTTGGTGGCATGCTGTAATGATGAGTGG 142
QY 1013 GACTGTGCC---AGCTGACTATATAAAAAAACAACAAACCTTATCCAAACACA 1068
DB 141 GAACGTGCCAGCATGTAACATATAAAAAAACAACAAACCTTATCCAAACACA 82
QY 1069 CTGTCCGTATGTAATGATGAGTCTGCGCCCACTGATCTCTTTGATGCTTGATGCT 1128
DB 81 CTGTCCGTATGTAATGATGAGTCTGCGCCCACTGATCTCTTTGATGCTTGATGCT 22
QY 1129 CTTTGTGTTGGGCTTGAGAA 1149
DB 21 CTTTGTGTTGGGCTTGAGAA 1

RESULT 15
US-10-027-632-196186/c
; Sequence 196186, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027, 632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218, 006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198, 676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193, 483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185, 218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167, 363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156, 358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146, 002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196186
; LENGTH: 559
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-196186

Query Match 14.1%; Score 428.2; DB 43; Length 559;
Best Local Similarity 92.2%; Pred. No. 2.7e-64;
Matches 517; Conservative 2; Mismatches 30; Indels 12; Gaps 6;
QY 599 ATTCTAACAATATTATGATTTATTTGATGATTTACATATTACATGTTGTTGA 658
DB 559 ATTCTAACAATATTATGATTTATTTGATGATTTACATATTACATGTTGTTGA 500
QY 659 CACAAATTTTAATATGTTCTTGATATGCAATATTTGCTTTAAATTTTAACTTCT 718
DB 499 CACAAATTTTAATATGTTCTTGATATGCAATATTTGCTTTAAATTTTAACTTCT 440
QY 719 TTAATTTACTTTGTTATAGTCTCACTATATTTCAAGTTTAAATTTAGATATTCAG 778
DB 439 TTAATTTACTTTGTTATAGTCTCACTATATTTCAAGTTTAAATTTAGATATTCAG 380

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QY 779 CCTTTAAATATTTCCTTAATTTTGTGACCTCTAATTTTAACTGTAAAT 838
    |||||
Db 379 -CTTTAAATATTTCCTTAATTTTGTGACCTCTAATTTTAACTGTAAAT 322
    |||||
QY 839 ATAGTCTGTATTGTGAAAGAGACTTTAGAAAGTGAATAAGATACCTTCACAAAATCTT -A 897
    |||||
Db 321 ACAGTTCTGTATTGTGAAAGAGACTTTAGAAAGTGAATAAGATACCTTCACAAAATCTTAA 262
    |||||
QY 898 AAAGACTTCTTGAGAGTCTGTAAAGAGAGATTAACATGTATACCTTATCTTTTCTTGCAAT 957
    |||||
Db 261 AAAGACTTCTTGAGAGTCTGTAAAGAGAGATTAACATGTATACCTTATCTTTTCTTGCA 202
    |||||
QY 958 GCC---ATGATCATCAGATGCTCATGCTCATGCTGCTGCTG-ATGATGAGTGG 1012
    |||||
Db 201 TGCATGAAATCATCAAAATGCAAGCTCATGTGTGTGCTGAAATGATGAGTGG 142
    |||||
QY 1013 GACTGTGCC---AGCTGAACATATAAAAAAAAAAAAAACAAACAAACCTTATCCAAACACA 1068
    |||||
Db 141 GAACGTGTGCCCACTGAACTATAAAAAAAAAAAAAACAAACAAACCTTATCCAAACACA 82
    |||||
QY 1069 CTGTCTCTGTATTGTATGATGATGCCCCAAGTGAATTTCTTTTGTATGCTTTGTGATTTGCT 1128
    |||||
Db 81 CTGTCTCTGTATTGTATGATGATGCCCCAAGTGAATTTCTTTTGTATGCTTTGTGATTTGCT 22
    |||||
QY 1129 CTTTGTGAGGCTTGAGAA 1149
    |||||
Db 21 CTTTGTGAGGCTTGAGAA 1
    |||||
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Search completed: April 10, 2004, 17:18:56
Job time : 8790 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 08:25:12 ; Search time 6908 Seconds
(without alignments)
1363.049 Million cell updates/sec

Title: US-09-430-412A-1
Perfect score: 3045
Sequence: 1 atccatcaataacccgtta.....gtggagagatgggctcttcg 3045

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_estcin:*
3: em_estcin:*
4: em_estcin:*
5: em_estcin:*
6: em_estcin:*
7: em_estcin:*
8: em_estcin:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estfun:*
17: em_estfun:*
18: em_estfun:*
19: em_estfun:*
20: em_estfun:*
21: em_estfun:*
22: em_estfun:*
23: em_estfun:*
24: em_estfun:*
25: em_estfun:*
26: em_estfun:*
27: em_estfun:*
28: gb_est1:*
29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	594	13.5	635	AG174550 Pan trogl
2	420	13.8	515	AG0885016 HS 5518 A
3	111.2	3.7	1101	AG0885016 HS 5518 A
4	108.6	3.6	475	AG0304345 HS_3176_B

C 5	107.2	3.5	1101	29	CNS00EVL	AL069706 Drosophila
C 6	103.6	3.4	1201	9	AL565455	AL565455
C 7	102	3.3	1056	13	BX415058	BX415058
C 8	101.4	3.3	1201	9	AL565455	AL565455
C 9	101	3.3	1165	13	BX338369	BX338369
C 10	100.8	3.3	714	28	AZ849216	AZ849216
C 11	100.4	3.3	1098	13	BX377526	BX377526
C 12	99.6	3.3	1200	13	BX415878	BX415878
C 13	99.2	3.3	1101	29	CNS00L72	AL078714 Drosophila
C 14	98.8	3.2	1272	28	CNS04939	CNS04939
C 15	98.4	3.2	1101	29	CNS0021J	AL061936 Drosophila
C 16	96	3.2	997	29	CNS005TE	AL060767 Drosophila
C 17	94.6	3.1	994	29	CNS04NOU	AL298972 Tetrahodon
C 18	94.2	3.1	1201	13	BX335216	BX335216
C 19	93.8	3.1	1201	13	BX458623	BX458623
C 20	93.8	3.1	1201	29	CNS057539	CNS057539
C 21	92.4	3.0	1101	29	CNS00807	AL069440 Drosophila
C 22	92.4	3.0	1101	29	CNS057970	CNS057970
C 23	92.2	3.0	1101	29	CNS0039G	AL063921 Drosophila
C 24	92	3.0	1200	13	BX437758	BX437758
C 25	91.8	3.0	1201	13	BX448679	BX448679
C 26	91.4	3.0	1200	13	BX437758	BX437758
C 27	91.2	3.0	872	14	CR022958	CR022958
C 28	91.2	3.0	1201	13	BX443774	BX443774
C 29	91	3.0	1045	13	BX456814	BX456814
C 30	90.6	3.0	1201	9	AL547503	AL547503
C 31	90.6	3.0	1201	13	BX357882	BX357882
C 32	90	3.0	987	29	CNS00418	AL066537 Drosophila
C 33	89.8	2.9	1052	13	BUS60001	BUS60001
C 34	89.2	2.9	1200	13	BX415878	BX415878
C 35	88.8	2.9	975	28	BH179465	BH179465
C 36	88.8	2.9	1201	9	AL536104	AL536104
C 37	88.8	2.9	1391	29	CG754863	CG754863
C 38	88.8	2.9	1392	29	CG757503	CG757503
C 39	88.6	2.9	1200	13	BX436510	BX436510
C 40	88.2	2.9	1101	29	CNS017RP	AL108415 Drosophila
C 41	88	2.9	1592	29	CG750135	CG750135
C 42	87.8	2.9	1201	13	BX443774	BX443774
C 43	87.8	2.9	1201	13	BX461824	BX461824
C 44	87.8	2.9	1350	29	CG744271	CG744271
C 45	87.4	2.9	1140	13	BX415974	BX415974

ALIGNMENTS

RESULT 1
AG174550/c
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-044N13.T1, genomic survey
ACCESSION
AG174550.1 GI:16704230
VERSION
AG174550.1
KEYWORDS
Pan troglodytes (chimpanzee)
SOURCE
Pan troglodytes
ORGANISM
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE
1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H., and Sakaki, Y.,
BAC end sequences of library RPCI-43
2 (bases 1 to 635)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Toto, Y., Watanabe, H., and Sakaki, Y.,
Direct Submission (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Saitama-shi, Saitama-shi, Japan
E-mail: chimpanzee@gs.riken.go.jp, URL: http://hsp.gsc.riken.go.jp/
Tel: 81-45-503-9111, Fax: 81-45-503-9170
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC

end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TU

LIBRARY

Vector 1 : PBACe3.6

R.site 1 : EcoRI

R.site 2 : EcoRI

Location/Qualifiers

FEATURES

source

1..635
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-044N13.TU"
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ORIGIN

Query Match 19.5%; Score 594; DB 29; Length 635;
Best Local Similarity 97.5%; Pred. No. 1.1e-91;
Matches 614; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

1973 GGTAAAGAGTCAAAAGGCGATGTGAATGCCAGGCTTCACTTAGAACATATGCAAA 2032
635 GGTAAAGAGTCAAAAGGCGATGTGAATGCCAGGCTTCACTTAGAACATATGCAAA 576
2033 TATTTCCATCCCTGAATTTACTAGCCACAAAGCTATGGAAGTGCAGTCACTGAAT 2092
575 TATTTCCATCCCTGAATTTACTAGCCACAAAGCTATGGAAGTGCAGTCACTGAAT 516
2093 TACAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2152
515 TACAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 456
2153 TTGTTCTTCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2212
455 TTGTTCTTCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 396
2213 AATTTGCTTCTCCCGGTTCCCAACGTTAAATAAAGTCAAGGCAATATTCCTCT 2272
395 AATTTGCTTCTCCCGGTTCCCAACGTTAAATAAAGTCAAGGCAATATTCCTCT 336
2273 GAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2332
335 GAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 276
2333 CGTTGTTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2392
275 CGTTGTTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 216
2393 GCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2452
215 GCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 156
2453 AGCAATATTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2512
155 AGCAATATTTGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 96
2513 CGTTTCTCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2572
95 CGTTTCTCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 36
2573 AATATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2602
35 AATATGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 7

RESULT 2
A0885016 515 bp DNA linear GSS 09-Nov99
LOCUS A0885016
DEFINITION HS 5518 A2 C02 T7A RPCI-11 Human Male BAC library Homo sapiens
genomic clone Plate=9286 Col=4 Row=E, genomic survey sequence.

ACCESSION A0885016
VERSION A0885016.1 GI:6315483
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 515)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., and Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE

99380589

PubMed

10449764

COMMENT

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACpac Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (<http://www.htsc.washington.edu>)
Plate: 9286 row: E column: 4
Seq primer: T7
Clas: BAC ends
High quality sequence stop: 515.

FEATURES

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/organism="Homo sapiens"
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/clone="Plate=9286 Col=4 Row=E"
/sex="male"
/clone_id="RPCI-11 Human Male BAC library"
/note="Vector: PBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoBI Methylase. Size selected DNA was cloned into the PBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match 13.8%; Score 420; DB 28; Length 515;
Best Local Similarity 96.2%; Pred. No. 6.7e-62;
Matches 459; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

1163 AATTCAGAGCTCAATTTGAACACATATTAAGATTATTCGAATCTAGTAATCTGTT 1222
32 AANNCAAGCTCAATTTGAACACATATTAAGATTATTCGAATCTAGTAATCTGTT 91
1223 CATGTTATCCAGTGTCACTCTTTGAGATTCATCTTCACTCAGGATGATC 1282
92 CATGTTATCCAGTGTCACTCTTTGAGATTCATCTTCACTCAGGATGATC 151
1283 AGGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1341
152 AGGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 211
1342 TTATCCATGCTCAAAATGATTAATTTG-TTCTGTTAAAGGAAGAGTTAGAAC 1400
212 TTATCCATGCTCAAAATGATTAATTTGTTTCTGTTAAAGGAAGAGTTAGAAC 271
1401 AAACCTTTGAATGATCTTTA-TTTCAGATATTAACATTTCCAAATGTTAATCATTTG 1459
272 AAACCTTTGAATGATCTTTA-TTTCAGATATTAACATTTCCAAATGTTAATCATTTG 331
1460 GAAATGCAATCATTCGTTCTCCCAAAAGAGTAAATTTAATGAGTTCCAAAGTTC 1519

Accession	Sequence	Position
D8	GAATGCAATGACTTCTTTCTTCCACAAAAGGTAATTTATGTCACTGCCAAAGTTC	391
QY	AGGTTATGACAGCAACAAAACCAACACAGGTGAAGTGTAGCTTAGCTTTATTTAAATGG	1579
D8	ACGTTATGACGCGACAAAACCAACACAGGTGAGATGTAGCTTAGCTTTATTTAAATGG	451
QY	CATCCCAAGTAGAAGTGTGTAATACAGATCTCAGAGCTTCCGAAGAAAGCTAAA	1636
D8	CATTCGCCACTTAGAAGCTTGTGTAATACAGATCTCCACGCTTTCTAAAGAAAGCTAAA	508

RESULT 3	CNS00EVL	LOCUS	DEFINITION
	CNS00EVL	1101 bp	DNA linear GSS 04-JUN-1999
			Drosophila melanogaster genome survey sequence T7 end of Bac:
			BACR29B23 of RPCT-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION	AL069706	GI:4949849
VERSION	AL069706.1	
KEYWORDS	GSS.	
SOURCE	Drosophila melanogaster (fruit fly)	
ORGANISM	Drosophila melanogaster	

REFERENCE
1 (bases 1 to 1101)

REFERENCE 1 (bases 1 to 1101)
AUTHORS Genoscope,
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ::

COMMENT

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazuhiro Oseegawa and Aaron Mammasser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RBC1-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACDPC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES	Location/Qualifiers
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/note="end : T7"

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 Best Local Similarity 35.7%; Pred. No. 3.3e-09;
 Matches 232; Conservative 127; Mismatches 286; Indels 5; Gaps 2

126 TTCTGTATCTTTAGAGTTAAACATGAGAAGATTGGCTAAGTGAAAATGAAATGAACGCA 189

Db 454 YTCGATWIMMMDDNNWAAITWNNAAWAAWTTATWAAATWAAAAAANNNWNTTTTTT 513

Qy 186 ATATCATCTTGCAATATATCATTTATTATATAATACACAGTATTATTAGTTTAAAAAGTTAAA 24

514 WWWIWAITTTTINAWITWIAIAAAAWATAITTTAAAWAAIAWATTAWAATT 573

Oy 246 CATAATATCATTTAAGCATGACATGSACCAATAGGSAACCTARCCRGTCGTGCGATACTT 308
 Db 574 TATAAAWWTATATTAATWTATATAAATWTATTAATATATAAAAAAATATTTTWTATAAATTT 633

Qy	306	TCGATCTCTGGTTCCCTCCCTGAGTATCCATTAAGTCGCCCTTGAAAAACGTTTAAATG	365
Db	634	TTAAATATTTAATT--AAATATTAAATTAATTAATTTAAATTTAAATTTAAATTTAAATTA	691
Qy	366	TAAAGAAATAAAAAGTTTGATATATATATGATATATTATTACTAAGAAAAAACTGTAAT	425
Db	692	AAAAAAAAAAAAAAATWAAWAAATWAAWAAATTAATTAATAAATAAATAAATAAATAA	751
Qy	426	TTGATTTTGGAAAACTTGATAAATCTCAAT---CATAGCATATGGAAGCAAGATPA	482
Db	752	TAATATWATPAATTAATTTATWTAATWTAATWTAATWTAATWTAATWTAATWTAATWTA	811
Qy	483	CAAAATGCTATACCTCAGGAATATTAATTCAGATTTTACAGATTTTAACTTCTTGATG	542
Db	812	WATWAAATWAAAWAAWAAATWAAATWAAATWAAATWAAWAAWAAWAAWAAWAAWAA	871
Qy	543	AGAAAAATATAATTTGTCAGTTATTTAAACATTTTGGATCCACAGATGAAAGCAATTC	602
Db	872	AWAAAAAATWAAATTTWTTTWTWAAWAAATATAAAMWAAWAAWAAWAAWAAWAAWAA	931
Qy	603	TAACTACATATTTATGATTTTATTTGATTTTCATATTACATGCTGTTTGACACA	662
Db	932	AAWAAWWTWATATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	991
Qy	663	ATTCTTATATATGTTCTGATATGACATATAATTGCTTCTTAAATTTTAAAGTTCCTTAT	722
Db	992	TATWTAATWTAATATTTATTTAAWAAATATTTTAAWAAWAAATTAATATWTAATWTAAT	1051
Qy	723	TTTACTTGTGTTAAGCTGCACATATAATTCGAAGTTTAAATTTAGATA	772
Db	1052	ATAAATAATTAATTTATATATWTAATWTAATWTAATWTAATWTAATWTAATWTAATW	1101

	LOCUS	DEFINITION	475 bp	DNA	linear	GSS 16--DEC-1998
RESULT 4	A0304345/c					
	A0304345	H5_3116_B2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=1176 Col=22 Row=P genomic survey				

ACCESSION	sequence,
VERSION	AQ304345
KEYWORDS	AQ304345.1 GI:4020182
SOURCE	GSS.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE AUTHORS
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 475)
Meharata, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.

TITLE	COMMENT
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)	
JOURNAL MEDLINE	
99380589	
PUBMED	
10449764	
Contact: Mahairas GG, Wallace JC, Hood L	

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel.: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Genetics, Tissue, Connective

```

FEATURES
source
sequence: ragged connective:
Plate: 3176 row: p column: 22
Class: BAC ends
High quality sequence stop: 475.
Location/Qualifiers
1. .475
/organism="Homo sapiens"

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/mol_type="genomic DNA"
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/clone="Plate=3176 Col=22 Row=P"
/sex="male"

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 08:35:04 ; Search time 238 Seconds

(Without alignments)
7100.107 Million cell updates/sec

Title: US-09-430-412A-1

Perfect score: 3045

Sequence: 1 atcatcatatataccttca.....gtgagagatggtctctcgcg 3045

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents NA.*
2: /cgm2_6/ptodata/2/ina/5A.COMB.seq.*
3: /cgm2_6/ptodata/2/ina/5B.COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6A.COMB.seq.*
5: /cgm2_6/ptodata/2/ina/6B.COMB.seq.*
6: /cgm2_6/ptodata/2/ina/Backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	125.6	4.1	7218	1	US-08-232-463-14
C 2	75.2	2.5	6317	4	US-10-204-708-11
C 3	74	2.4	665	2	US-08-883-795A-36
C 4	68.6	2.3	636	3	US-08-998-416-1137
C 5	68.4	2.2	640681	4	US-09-790-988-1
C 6	67.8	2.2	53526	3	US-08-658-136-2
C 7	67.8	2.2	53577	3	US-08-658-136-1
C 8	65.2	2.1	507	4	US-09-489-039A-1200
C 9	65.2	2.1	516	4	US-09-489-039A-1064
C 10	65.2	2.1	549	4	US-09-489-039A-1065
C 11	65.2	2.1	537	4	US-09-489-039A-1130
C 12	65.2	2.1	558	4	US-09-488-039A-1011
C 13	65.2	2.1	609	4	US-09-488-039A-1177
C 14	64.4	2.1	1866	3	US-09-173-581-13
C 15	64.4	2.1	1866	3	US-09-420-915-13
C 16	63.8	2.1	19124	2	US-08-487-826B-13
C 17	63.4	2.1	10640	4	US-09-417-485D-5
C 18	63.2	2.1	11049	4	US-10-204-708-21
C 19	62.8	2.1	819	4	US-09-918-686-5
C 20	62.8	2.1	92139	4	US-09-918-686-1
C 21	62.4	2.0	6866	4	US-10-204-708-20
C 22	62.2	2.0	1268	4	US-09-369-247-42
C 23	62	2.0	615	3	US-08-998-416-186
C 24	62	2.0	319608	4	US-09-539-333D-1
C 25	61.8	2.0	1867	3	US-09-679-409-1
C 26	61.8	2.0	24183	3	US-08-943-731-11
C 27	61.8	2.0	24183	3	US-08-943-731-3

C 28	61.8	2.0	202001	4	US-09-734-674-3	Sequence 3, Appl
C 29	61.6	2.0	837	3	US-08-998-416-28	Sequence 288, App
C 30	61.4	2.0	685	2	US-08-883-795A-36	Sequence 36, Appl
C 31	60.6	2.0	685	4	US-09-183-266A-16	Sequence 16, Appl
C 32	60.6	2.0	7122	3	US-09-318-448-2	Sequence 2, Appl
C 33	60.6	2.0	7122	4	US-09-347-878-4	Sequence 4, Appl
C 34	60.6	2.0	40000	4	US-09-780-049-18	Sequence 18, Appl
C 35	60.2	2.0	5852	1	US-07-867-106-2	Sequence 2, Appl
C 36	60.2	2.0	13205	4	US-09-835-811-3	Sequence 3, Appl
C 37	60.2	2.0	640681	4	US-10-204-708-80	Sequence 1, Appl
C 38	59.8	2.0	8961	4	US-09-641-638-651	Sequence 80, Appl
C 39	59.6	2.0	20674	4	US-09-641-638-651	Sequence 651, App
C 40	59.2	1.9	396	4	US-09-640-173-53	Sequence 53, Appl
C 41	59.2	1.9	396	4	US-09-713-550-53	Sequence 2, Appl
C 42	59	1.9	10467	4	US-10-204-708-2	Sequence 6, Appl
C 43	59	1.9	20303	1	US-08-370-975B-6	Sequence 1, Appl
C 44	59	1.9	26764	1	US-08-370-975B-1	Sequence 3, Appl
C 45	59	1.9	148567	4	US-09-801-876B-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEFAX: (703)833-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT99T-Fls
US-08-232-463-14
Query Match 4.1%, Score 125.6, DB 1, Length 7218:

Best Local Similarity 2.1%; Pred. No. 4.3e-18;
Matches 8; Conservative 284; Mismatches 88; Indels 0; Gaps 0;

QY	2665	TGAGCTGACCGGGAGGATCTGGGTGTGAAGAATTCTGAGTCTCTTGACAAAA	2724
Db	1441	TTGGTAACRRR	1382
QY	2725	GAGACTGCATGCCAAGAAGCTGAGCTAGAGGAGAGAGGCGGGACCAGAGAAAG	2784
Db	1381	RR	1322
QY	2785	AAGCACTCTCGGGGTTGGGAGTAGTATTAGAGGGGAGGTTGAGTGGAGGAAAGAG	2844
Db	1321	RR	1262
QY	2845	CTGGGTTTCGAAGGCACTCAGAGGATTAATAAAGGAAGTGGAGGAAGGAG	2904
Db	1261	RR	1202
QY	2905	ACTGAAGGGAAGCAGGTGGGGAGAAAGGGACGAAAGAGCAGAGAGAGAGAGA	2964
Db	1201	RR	1142
QY	2965	GGAGGAGAGAGGGGAGAGAGGGAAGAGGAAATAGCGAGAGAGGTCACAGCTCAC	3024
Db	1141	RR	1082
QY	3025	CGTGAAGATGGGCTCTC 3044	
Db	1081	RRRRRRRRRRRRBATCC 1062	

RESULT 2
US-10-204-708-11

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Sequence ID: Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
Applicant: OLEK, Alexander
Applicant: PIEPENBROCK, Christian
Applicant: BERLIN, Kurt
Title of Invention: Diagnosis of Diseases Associated with DNA Replication
Title of Invention: By Assessing DNA Methylation
File Reference: 5013.1012
Current Application Number: US/10/204,708
Current Filing Date: 2003-05-06
Prior Application Number: PCT/EP01/03971
Prior Filing Date: 2001-04-06
Prior Application Number: DE 10019058.8
Prior Filing Date: 2000-04-06
Prior Application Number: DE 10019173.8
Prior Filing Date: 2000-04-07
Prior Application Number: DE 10032529.7
Prior Filing Date: 2000-06-30
Prior Application Number: DE 10043826.1
Prior Filing Date: 2000-09-01
Number of Seq ID Nos: 98
Seq ID No 11
Length: 6317
Type: DNA
Organism: Artificial Sequence
Feature:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-11

```

Query Match	2.5%;	Score 75.2;	DB 4;	Length 6317;
Best Local Similarity	45.0%;	Pred. No. 4.4e-07;		
Matches 391;	Conservative	5;	Mismatches 458;	Indels 14;
				Gaps 3;

QY 2 ATATCAATAAATATCCGTAATTAAGCTGCTTTCTTTAGGTAACTTGTAGAGGCTTAA 60
Db 1201 ATTGTAGAGTATATTATTATTAATTTTTTATTATGTTTAAATAGTAAAGTATATTTT 1260
QY 61 AGAATTAAGACTCATCTTTTACAGAGGCTTTGGTTGCAGCATTTACTTAAGAAATATT 120

Db	1261	ATTGGAGATAATTTTTTATTATAGAAAAGCATTTAATAATGATTTTTTTTATAGAGGAT	1320
Oy	121	TGGATTCTGATCTTTAAGAGTTAAACATAGAAAGATTGGCTAAGGAAATCAATGAA	180
Db	1321	TAAATTTTGGTAGTAGAGAGATTAAGAAAAAAATTTATTTATTAATAAAAAAATTAATTT	1380
Oy	181	ACGCATATCATCTCGCATATATCATTTATTTATATCAAGATTTTATGTTTAAAG	240
Db	1381	ATAAATAATGATTATTTTATTTATAGTAATATGTTATATATGTAATATGTAATATTT	1440
Oy	241	TTAAACATTAATATCTTTATATGTCATTGASAGATTAGTGAACCTA--RCRGTGTCG	297
Db	1441	TTTGAAGAAATTTATTTTTTTATGCTGTAATTTTTTTATATAAAATTAATATAGTACTTTT	1500
Oy	298	GAATATCTTGATACCTCTGTTTCCCTCCTAGATTCATATAGTGGCTTTGAAAACGT	357
Db	1501	GTTAAATTTTATTTTATTTGATTTTGTAGAAATTAATATATATGTTTTTTGTAAAAAGTTT	1560
Oy	358	TTAAATTTGTAAGAAATTAATATGTTTGTATATTTATGTAATTTATTTACTAGAAAAACTT	417
Db	1561	TAGAAATTTAGATTAATTTATTTAATTAAGTTTATTTTATTTATTTTATGATAAATTTTTT	1620
Oy	418	GAATTACTTTGATTTTGAAAAACTTTGATTAATTTCAATCATAGCATATTTGAAGCAAG	477
Db	1621	AAATATATAGAAATTTGAAGAGATTTGTTATTAATAATATTTATTAATGATTAAGATTTAT	1680
Oy	478	AATACCAATGCTATACCTCAG-----AATATTAATCCAGATTTTACAGCAATTT	529
Db	1681	AATGTTAATATTTTGCGATGATTAATTAATTTTATTTTATTTTATGATTAATTAATTT	1740
Oy	530	AACTTTCTGATGGAATAAATAATTTGTCAGTATTTAACTATTTGATCCCAACGAT	589
Db	1741	TAAAGTATTTATTAATATTTATTAAGATATTTTATTTTAAATATTTTGATATGTAATTTT	1800
Oy	590	GAAGCAATTTCTACATCAATATTTATGATTTATTTTGATTTTACATATTAACATGT	649
Db	1801	AAGGTATAGGATAATTTATATAGATATATTAATTTAATTAATTTAAGAAATTTTATPA	1860
Oy	650	GTTGTTGACCAATTTCTATATATATGTTCTGATATAGCATATATTTGTTCTTAATTT	709
Db	1861	TTTTTTAATATTAATTGAATAATTAATTTTTTTTATTTTATTTATGTTTAAAGTTTTTA	1920
Oy	710	AAGTTCCCTAATTTTACTTGTATTAGTCTCACTATAATTTCAAGATTTAATTTTAG	769
Db	1921	TAGTATTTTGTGATTAAGATTTTATTAATTAAGTTATATATATGTAATTTGATTTTAT	1980
Oy	770	ATTAATCAGCCTTTAAATATTTTCCCATTAATAATTTTGAGACCTCAACTCATTTTTA	829
Db	1981	ATACT--GTTTTGAGTTTTTTTATTTTTTTTTTTTTTTTTTTTATATGTTTTTATA	2037
Oy	830	ACGTAAATATAGTCTGATTTTGGA	857
Db	2038	GATTTATGAGCTAATTTATTTGTAA	2065

RESULT 3

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/ US-06-063-7524-587/
/ Sequence 36, Application US/06863795A
/ Patent No. 5985607
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Delcive, Genevieve
/ APPLICANT: Awang, Gregor
/ TITLE OF INVENTION: Recombinant DNA Molecules and Expression
/ TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
/
/ NUMBER OF SEQUENCES: 39
/
/ CORRESPONDENCE ADDRESS:
/
/ ADDRESSEE: BERSKIN & PARR
/ STREET: 40 King Street West
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/
/ ZIP: M5H 3Y2
/
/

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